

**This Page Is Inserted by IFW Operations
and is not a part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- **BLACK BORDERS**
- **TEXT CUT OFF AT TOP, BOTTOM OR SIDES**
- **FADED TEXT**
- **ILLEGIBLE TEXT**
- **SKEWED/SLANTED IMAGES**
- **COLORED PHOTOS**
- **BLACK OR VERY BLACK AND WHITE DARK PHOTOS**
- **GRAY SCALE DOCUMENTS**

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ :		A2	(11) International Publication Number:	WO 98/11225
C12N 15/19, C07K 14/715, A61K 38/17, C07K 16/18, A01K 67/027			(43) International Publication Date:	19 March 1998 (19.03.98)
(21) International Application Number:	PCT/GB97/02479			
(22) International Filing Date:	11 September 1997 (11.09.97)			
(30) Priority Data:	PO 2246	11 September 1996 (11.09.96)	AU	
(71) Applicant (for all designated States except US):	AMRAD OPERATIONS PTY. LTD. [AU/AU]; 576 Swan Street, Richmond, VIC 3121 (AU).			
(71) Applicant (for GB only):	DZIEGLEWSKA, Hanna, Eva [GB/GB]; Frank B. Dehn & Co., 179 Queen Victoria Street, London EC4V 4EL (GB).			
(72) Inventors; and				
(75) Inventors/Applicants (for US only):	HILTON, Douglas, James [AU/AU]; 244 Research Road, Warrandyte, VIC 3113 (AU). NICOLA, Nicos, Antony [AU/AU]; 56 Churchill Avenue, Mont Albert, VIC 3127 (AU). FARLEY, Alison [AU/AU]; 279-19 Miller Street, North Fitzroy, VIC 3068 (AU). WILLSON, Tracy [AU/AU]; 26 Fortuna Avenue, North Balwyn, VIC 3104 (AU). ZHANG, Jian-Guo [CN/AU]; 3 Karri Crescent, Hoppers Crossing, VIC 3029 (AU). ALEXANDER, Warren [AU/AU]; 13 Park Street, Moonee Ponds, VIC 3039 (AU). RAKAR, Steven [AU/AU]; 26 Riverside			
				Avenue, Avondale Heights, VIC 3034 (AU). FABRI, Louis [AU/AU]; 8 Laver Court, Mill Park, VIC 3082 (AU). KOJIMA, Tetsuo [JP/JP]; 1-8-1-302 Minami-Rokugou, Ota-ku, Tokyo 144 (JP). MAEDA, Masatsugu [JP/JP]; 1-6-2-606 Kasuga, Tsukuba, Ibaraki 305 (JP). KIKUCHI, Yasufumi [JP/JP]; 1-29-5-110 Komatsu, Tsuchiura, Ibaraki 300 (JP). NASH, Andrew [AU/AU]; 24 Green Street, Northcote, VIC 3070 (AU).
				(74) Agents: DZIEGLEWSKA, Hanna, Eva et al.; Frank B. Dehn & Co., 179 Queen Victoria Street, London EC4V 4EL (GB).
				(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).
				Published Without international search report and to be republished upon receipt of that report.

(54) Title: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME

(57) Abstract

The present invention relates generally to a novel haemopoietin receptor or derivatives thereof and to genetic sequences encoding same. Interaction between the novel receptor of the present invention and a cytokine ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The novel receptor and its derivatives and the genetic sequences encoding same of the present invention are useful in the development of a wide range of agonists, antagonists, therapeutics and diagnostic reagents based on ligand interaction with its receptor.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

**A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC
SEQUENCES ENCODING SAME**

The present invention relates generally to a novel
5 haemopoietin receptor or derivatives thereof and to
genetic sequences encoding same. Interaction between
the novel receptor of the present invention and a ligand
facilitates proliferation, differentiation and survival
10 of a wide variety of cells. The novel receptor and its
derivatives and the genetic sequences encoding same of
the present invention are useful in the development of a
wide range of agonists, antagonists, therapeutics and
diagnostic reagents based on ligand interaction with its
receptor.

15 Bibliographic details of the publications numerically
referred to in this specification are collected at the
end of the description. Sequence Identity Numbers (SEQ
ID NOS.) for the nucleotide and amino acid sequences
20 referred to in the specification are defined following
the bibliography.

Throughout this specification and the claims which
follow, unless the context requires otherwise, the word
25 "comprise", or variations such as "comprises" or
"comprising", will be understood to imply the inclusion
of a stated integer or group of integers but not the
exclusion of any other integer or group of integers.

30 The rapidly increasing sophistication of recombinant DNA
techniques is greatly facilitating research into the
medical and allied health fields. Cytokine research is
of particular importance, especially as these molecules
regulate the proliferation, differentiation and function
35 of a wide variety of cells. Administration of
recombinant cytokines or regulating cytokine function
and/or synthesis is becoming increasingly the focus of

medical research into the treatment of a range of disease conditions.

Despite the discovery of a range of cytokines and other secreted regulators of cell function, comparatively few cytokines are directly used or targeted in therapeutic regimens. One reason for this is the pleiotropic nature of many cytokines. For example, interleukin (IL)-11 is a functionally pleiotropic molecule (1,2), initially characterized by its ability to stimulate proliferation of the IL-6-dependent plasmacytoma cell line, T11 65 (3). Other biological actions of IL-11 include induction of multipotential haemopoietin progenitor cell proliferation (4,5,6), enhancement of megakaryocyte and platelet formation (7,8,9,10), stimulation of acute phase protein synthesis (11) and inhibition of adipocyte lipoprotein lipase activity (12, 13).

Other important cytokines in the IL-11 group include IL-6, leukaemia inhibitory factor (LIF), oncostatin M (OSM) and CNTF. All these cytokines exhibit pleiotropic properties with significant activities in proliferation, differentiation and survival of cells. Members of the haemopoietin receptor family are defined by the presence of a conserved amino acid domain in their extracellular region. However, despite the low level of amino acid sequence conservation between other haemopoietin receptor domains of different receptors, they are all predicted to assume a similar tertiary structure, centred around two fibronectin-type III repeats (18,19).

The size of the haemopoietin receptor family has now become extensive and includes the cell surface receptors for many cytokines including interleukin-2 (IL-2), IL-3, IL-4, IL-5, IL-6, IL-7, IL-9, IL-11, IL-12, IL-13, IL-15, granulocyte colony stimulating factor (G-CSF), granulocyte-macrophage-CSF (GM-CSF), erythropoietin,

thrombopoietin, leptin, leukaemia inhibitory factor, oncostatin-M, ciliary neurotrophic factor, cardiotrophin, growth hormone and prolactin. Although most of the members of the haemopoietin receptor family act as classic cell surface receptors, binding their cognate ligand at the cell surface and initiating intracellular signal transduction, some receptors are also produced in naturally occurring soluble forms. These soluble receptors can either act as cytokine antagonists, by binding to cytokines and inhibiting productive interactions with cell surface receptors (eg LIF binding protein; (20) or as agonists, binding to cytokine and potentiating interaction with cell surface receptor components (eg soluble interleukin-6 receptor α-chain; (21)). Still other members of the family appear to be produced only as secreted proteins, with no evidence of a cell surface form. In this regard, the IL-12 p40 subunit is a useful example. The cytokine IL-12 is secreted as a heterodimer composed of a p35 subunit which shows similarity to cytokines such as IL-6 (22) and a p40 subunit which shares similarity with the IL-6 receptor α-chain (23). In this case the soluble receptor acts as part of the cytokine itself and essential to formation of an active protein. In addition to acting as cytokines (eg IL-12p40), cytokine agonists (eg IL-6 receptor α-chain) or cytokine antagonists (LIF binding protein), members of the haemopoietin receptor have been useful in the discovery of small molecule cytokine mimetics. For example, the discovery of peptide mimetics of two commercially valuable cytokines, erythropoietin and thrombopoietin, centred on the selection of peptides capable of binding to soluble versions of the erythropoietin and thrombopoietin receptors (24,25). Due to the importance and multifactorial nature of these cytokines, there is a need to identify receptors, including both cell bound and soluble, for pleiotropic cytokines. Identification

of such receptors permits the identification of pleiotropic cytokines and the development of a range of therapeutic and diagnostic agents.

5 Accordingly, one aspect of the present invention relates to a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a novel haemopoietin receptor or a derivative thereof.

10 More particularly, the present invention provides a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a novel haemopoietin receptor or a derivative thereof having the motif:

15 Trp Ser Xaa Trp Ser [SEQ ID NO:1],
wherein Xaa is any amino acid and is preferably Asp or Glu.

20 Even more particularly, the present invention is directed to a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a novel haemopoietin receptor or a derivative thereof, said receptor comprising the motif:

25 Trp Ser Xaa Trp Ser [SEQ ID NO:1]

wherein Xaa is any amino acid and is preferably Asp or Glu, said nucleic acid molecule is identifiable by
30 hybridisation to said molecule under low stringency conditions at 42EC with

5N (A/G)CTCCA(A/G)TC(A/G)CTCCA 3N [SEQ ID NO:7]
and

5N (A/G)CTCCA(C/T)TC(A/G)CTCCA 3N [SEQ ID NO:8].

35 Still more particularly, the present invention provides an isolated nucleic acid molecule comprising a sequence

of nucleotides substantially as set forth in SEQ ID NO:12 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:12 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

In a related embodiment, the present invention provides
10 an isolated nucleic acid molecule comprising a sequence
of nucleotides substantially as set forth in SEQ ID
NO:14 or a nucleotide sequence having at least 60%
similarity to the nucleotide sequence set forth in SEQ
ID NO:14 or a nucleotide sequence capable of hybridising
15 thereto under low stringency conditions at 42EC and
wherein said nucleotide sequence encodes a novel
haemopoietin receptor or a derivative thereof.

In another related embodiment, the present invention
20 provides an isolated nucleic acid molecule comprising a
sequence of nucleotides substantially as set forth in
SEQ ID NO:16 or a nucleotide sequence having at least
60% similarity to the nucleotide sequence set forth in
SEQ ID NO:16 or a nucleotide sequence capable of
25 hybridising thereto under low stringency conditions at
42EC and wherein said nucleotide sequence encodes a
novel haemopoietin receptor or a derivative thereof.

In a further related embodiment, the present invention
30 provides an isolated nucleic acid molecule comprising a
sequence of nucleotides substantially as set forth in
SEQ ID NO:18 or a nucleotide sequence having at least
60% similarity to the nucleotide sequence set forth in
SEQ ID NO:18 or a nucleotide sequence capable of
35 hybridising thereto under low stringency conditions at
42EC and wherein said nucleotide sequence encodes a
novel haemopoietin receptor or a derivative thereof.

In yet a further related embodiment, the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:24 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:24 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

Still yet a further embodiment of the present invention is directed to a sequence of nucleotides substantially as set forth in SEQ ID NO:28 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:28 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

In still yet another embodiment, the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides substantially set forth in SEQ ID NO:38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:38 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

The term "receptor" is used in its broadest sense and includes any molecule capable of binding, associating or otherwise interacting with a ligand. Generally, the interaction will have a signalling effect although the present invention is not necessarily so limited. For example, the "receptor" may be in soluble form, often

referred to as a cytokine binding protein. A receptor may be deemed a receptor notwithstanding that its ligand or ligands has or have not been identified.

5 Preferably, the novel receptor is derived from a mammal or a species of bird. Particularly, preferred mammals include humans, primates, laboratory test animals (e.g. mice, rats, rabbits, guinea pigs), livestock animals (e.g. sheep, horses, pigs, cows), companion animals (e.g. dogs, cats) or captive wild animals (e.g. deer, foxes, kangaroos). Although the present invention is exemplified with respect to mice, the scope of the subject invention extends to all animals and in particular humans.

15 The present invention is predicated in part on an ability to identify members of the haemopoietin receptor family with limited sequence similarity. Based on this approach, a genetic sequence has been identified in accordance with the present invention which encodes a novel receptor. The expressed genetic sequence is referred to herein as "NR6". Different forms of NR6 are referred to as, for example, NR6.1, NR6.2 and NR6.3. The nucleotide and corresponding amino acid sequences for these molecules are represented in SEQ ID NOS:12, 14 and 16, respectively.

30 Preferred human and murine nucleic acid sequences for NR6 or its derivatives include sequences from brain, liver, kidney, neonatal, embryonic, cancer or tumour-derived tissues.

35 Reference herein to a low stringency at 42EC includes and encompasses from at least about 1% v/v to at least about 15% v/v formamide and from at least about 1M to at least about 2M salt for hybridisation, and at least about 1M to at least about 2M salt for washing

conditions. Alternative stringency conditions may be applied where necessary, such as medium stringency, which includes and encompasses from at least about 16% v/v to at least about 30% v/v formamide and from at 5 least about 0.5M to at least about 0.9M salt for hybridisation, and at least about 0.5M to at least about 0.9M salt for washing conditions, or high stringency, which includes and encompasses from at least about 31% v/v to at least about 50% v/v formamide and from at 10 least about 0.01M to at least about 0.15M salt for hybridisation, and at least about 0.01M to at least about 0.15M salt for washing conditions.

15 The nucleic acid molecules contemplated by the present invention are generally in isolated form and are preferably cDNA or genomic DNA molecules. In a particularly preferred embodiment, the nucleic acid molecules are in vectors and most preferably expression vectors to enable expression in a suitable host cell. 20 Particularly useful host cells include prokaryotic cells, mammalian cells, yeast cells and insect cells. The cells may also be in the form of a cell line.

25 Accordingly, another aspect of the present invention provides an expression vector comprising a nucleic acid molecule encoding the novel haemopoietin receptor or a derivative thereof as hereinbefore described, said expression vector capable of expression in a selected host cell.

30 Another aspect of the present invention contemplates a method for cloning a nucleotide sequence encoding NR6 or a derivative thereof, said method comprising searching a nucleotide data base for a sequence which encodes the 35 amino acid sequence set forth in SEQ ID NO:1, designing one or more oligonucleotide primers based on the nucleotide sequence located in the search, screening a

nucleic acid library with said one or more oligonucleotides and obtaining a clone therefrom which encodes said NR6 or part thereof.

5 Once a novel nucleotide sequence is obtained as indicated above encoding NR6, oligonucleotides may be designed which bind cDNA clones with high stringency. Direct colony hybridisation may be employed or PCR amplification may be used. The use of oligonucleotide primers which bind under conditions of high stringency ensures rapid cloning of a molecule encoding the novel NR6 and less time is required in screening out cloning artefacts. However, depending on the primers used, low or medium stringency conditions may also be employed.

10 15 Alternatively, a library may be screened directly such as using oligonucleotides set forth in SEQ ID NO:7 or SEQ ID NO:8 or a mixture of both oligonucleotides may be used. In addition, one or more of oligonucleotides defined in SEQ ID NO:2 to 11 may also be used.

20 Preferably, the nucleic acid library is a cDNA, genomic, cDNA expression or mRNA library.

25 Preferably, the nucleic acid library is a cDNA expression library.

30 35 Preferably, the nucleotide data base is of human or murine origin and of brain, liver, kidney, neo-natal tissue, embryonic tissue, tumour or cancer tissue origin.

Preferred percentage similarities to the reference nucleotide sequences include at least about 70%, more preferably at least about 80%, still more preferably at least about 90% and even more preferably at least about 95% or above.

Another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haemopoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:13 or having at least about 50% similarity to all or part thereof.

Still yet another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haemopoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:15 or having at least about 50% similarity to all or part thereof.

Even yet another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haemopoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:17 or having at least about 50% similarity to all or part thereof.

A further aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haemopoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:19 or having at least about 50% similarity to all or part thereof.

Even yet another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haemopoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:25 or having at least about 50% similarity to all or part thereof.

Another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of

nucleotides encoding a novel haemopoietin receptor or derivative thereof having an amino acid sequence as set forth in one or more of SEQ ID NOs:29 or having at least about 50% similarity to all or part thereof.

5

Preferably, the percentage amino acid similarity is at least about 60%, more preferably at least about 70%, even more preferably at least about 80-85% and still even more preferably at least about 90-95% or greater.

10

The NR6 polypeptide contemplated by the present invention includes, therefore, derivatives which are components, parts, fragments, homologues or analogues of the novel haemopoietin receptors which are preferably encoded by all or part of a nucleotide sequences substantially set forth in SEQ ID NO:12 or 14 or 16 or 18 or 25 or 20 or 24 or 28 or 38 or a molecule having at least about 60% nucleotide similarity to all or part thereof or a molecule capable of hybridising to the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 20 or 24 or 28 or 38 or a complementary form thereof. The NR6 molecule may be glycosylated or non-glycosylated. When in glycosylated form, the glycosylation may be substantially the same as naturally occurring haemopoietin receptor or may be a modified form of glycosylation. Altered or differential glycosylation states may or may not affect binding activity of the novel receptor.

20

The NR6 haemopoietin receptor may be in soluble form or may be expressed on a cell surface or conjugated or fused to a solid support or another molecule.

30

As stated above, the present invention further contemplates a range of derivatives of NR6. Derivatives include fragments, parts, portions, mutants, homologues and analogues of the NR6 polypeptide and corresponding

genetic sequence. Derivatives also include single or multiple amino acid substitutions, deletions and/or additions to NR6 or single or multiple nucleotide substitutions, deletions and/or additions to the genetic sequence encoding NR6. "Additions" to amino acid sequences or nucleotide sequences include fusions with other peptides, polypeptides or proteins or fusions to nucleotide sequences. Reference herein to ANR6" includes reference to all derivatives thereof including functional derivatives or NR6 immunologically interactive derivatives.

Analogues of NR6 contemplated herein include, but are not limited to, modification to side chains, incorporating of unnatural amino acids and/or their derivatives during peptide, polypeptide or protein synthesis and the use of crosslinkers and other methods which impose conformational constraints on the proteinaceous molecule or their analogues.

Examples of side chain modifications contemplated by the present invention include modifications of amino groups such as by reductive alkylation by reaction with an aldehyde followed by reduction with NaBH₄; amidination with methylacetimidate; acylation with acetic anhydride; carbamoylation of amino groups with cyanate; trinitrobenzylolation of amino groups with 2, 4, 6-trinitrobenzene sulphonic acid (TNBS); acylation of amino groups with succinic anhydride and tetrahydrophthalic anhydride; and pyridoxylation of lysine with pyridoxal-5-phosphate followed by reduction with NaBH₄.

The guanidine group of arginine residues may be modified by the formation of heterocyclic condensation products with reagents such as 2,3-butanedione, phenylglyoxal and glyoxal.

The carboxyl group may be modified by carbodiimide activation via O-acylisourea formation followed by subsequent derivitisation, for example, to a corresponding amide.

5

Sulphydryl groups may be modified by methods such as carboxymethylation with iodoacetic acid or iodoacetamide; performic acid oxidation to cysteic acid; formation of a mixed disulphides with other thiol compounds; reaction with maleimide, maleic anhydride or other substituted maleimide; formation of mercurial derivatives using 4-chloromercuribenzoate, 4-chloromercuriphenylsulphonic acid, phenylmercury chloride, 2-chloromercuri-4-nitrophenol and other mercurials; carbamoylation with cyanate at alkaline pH.

10

15

20

Tryptophan residues may be modified by, for example, oxidation with N-bromosuccinimide or alkylation of the indole ring with 2-hydroxy-5-nitrobenzyl bromide or sulphenyl halides. Tyrosine residues on the other hand,

may be altered by nitration with tetrannitromethane to form a 3-nitrotyrosine derivative.

25

Modification of the imidazole ring of a histidine residue may be accomplished by alkylation with iodoacetic acid derivatives or N-carbethoxylation with diethylpyrocarbonate.

30

35

Examples of incorporating unnatural amino acids and derivatives during peptide synthesis include, but are not limited to, use of norleucine, 4-amino butyric acid, 4-amino-3-hydroxy-5-phenylpentanoic acid, 6-aminohexanoic acid, t-butylglycine, norvaline, phenylglycine, ornithine, sarcosine, 4-amino-3-hydroxy-6-methylheptanoic acid, 2-thienyl alanine and/or D-isomers of amino acids. A list of unnatural amino acid, contemplated herein is shown in Table 1.

These types of modifications may be important to stabilise NR6 if administered to an individual or for use as a diagnostic reagent.

- 5 Crosslinkers can be used, for example, to stabilise 3D conformations, using homo-bifunctional crosslinkers such as the bifunctional imido esters having $(CH_2)_n$ spacer groups with n=1 to n=6, glutaraldehyde, N-hydroxysuccinimide esters and hetero-bifunctional
- 10 reagents which usually contain an amino-reactive moiety such as N-hydroxysuccinimide and another group specific-reactive moiety such as maleimido or dithio moiety (SH) or carbodiimide (COOH). In addition, peptides can be conformationally constrained by, for example,
- 15 incorporation of C^α and N^ε-methylamino acids, introduction of double bonds between C^α and C^β atoms of amino acids and the formation of cyclic peptides or analogues by introducing covalent bonds such as forming an amide bond between the N and C termini, between two
- 20 side chains or between a side chain and the N or C terminus.

TABLE 1

	Non-conventional amino acid	Code	Non-conventional amino acid	Code
5	aminobutyric acid	Abu	L-N-methylalanine	Nmala
	Amino-"-methylbutyrate	Mgabu	L-N-methylarginine	Nmarg
	aminocyclopropane- carboxylate	Cpro	L-N-methyleasparagine	Nmasn
10	aminoisobutyric acid	Aib	L-N-methylcysteine	Nmcys
	aminonorbornyl- carboxylate	Norb	L-N-methylglutamine	Nmgln
	cyclohexylalanine		L-N-methylglutamic acid	Nmglu
	cyclopentylalanine	Cpen	Chexal-N-methylhistidine	Nmhis
15	D-alanine	Dal	L-N-methylisoleucine	Nmile
	D-arginine	Darg	L-N-methyllysine	Nmlys
	D-aspartic acid	Dasp	L-N-methylmethionine	Nmmet
	D-cysteine	Dcys	L-N-methylnorleucine	Nmnle
	D-glutamine	Dgln	L-N-methylnorvaline	Nmnva
20	D-glutamic acid	Dglu	L-N-methylornithine	Nmorn
	D-histidine	Dhis	L-N-methylphenylalanine	Nmphe
	D-isoleucine	Dile	L-N-methylproline	Nmpro
	D-leucine	Dleu	L-N-methylserine	Nmser
	D-lysine	Dlys	L-N-methylthreonine	Nmthr
25	D-methionine	Dmet	L-N-methyltryptophan	Nmtrp
	D-ornithine	Dorn	L-N-methyltyrosine	Nmtyr
	D-phenylalanine	Dphe	L-N-methylvaline	Nmval
	D-proline	Dpro	L-N-methylethylglycine	Nmetg
	D-serine	Dser	L-N-methyl-t-butylglycine	Nmtbug
30	D-threonine	Dthr	L-norleucine	Nle
	D-tryptophan	Dtrp	L-norvaline	Nva
	D-tyrosine	Dtyr	"-methyl-aminoisobutyrate	Maib
	D-valine	Dval	"-methyl-(-aminobutyrate	Mgabu
	D-"-methylalanine	Dmala	"-methylcyclohexylalanine	Mchexa
35	D-"-methylarginine	Dmarg	"-methylcyclopentylalanine	Mcpen
	D-"-methylasparagine	Dmasn	"-methyl-"-napthylalanine	Manap
	D-"-methylaspartate	Dmasp	"-methylpenicillamine	Mpen

	D- ² -methylcysteine	Dmcys	N-(4-aminobutyl)glycine	Nglu
	D- ² -methylglutamine	Dmgln	N-(2-aminoethyl)glycine	Naeg
	D- ² -methylhistidine	Dmhis	N-(3-aminopropyl)glycine	Norn
	D- ² -methylisoleucine	Dmile	N-amino- ² -methylbutyrate	Nmaabu
5	D- ² -methylelleucine	Dmleu	"-naphylalanine	Anap
	D- ² -methyllysine	Dmlys	N-benzylglycine	Nphe
	D- ² -methylmethionine	Dmmet	N-(2-carbamylethyl)glycine	Ngln
	D- ² -methylornithine	Dmorn	N-(carbamylmethyl)glycine	Nasn
	D- ² -methylphenylalanine	Dmphe	N-(2-carboxyethyl)glycine	Nglu
10	D- ² -methylproline	Dmpro	N-(carboxymethyl)glycine	Nasp
	D- ² -methylserine	Dmser	N-cyclobutylglycine	Ncbut
	D- ² -methylthreonine	Dmthr	N-cycloheptylglycine	Nchep
	D- ² -methyltryptophan	Dmtrp	N-cyclohexylglycine	Nchex
	D- ² -methyltyrosine	Dmty	N-cyclodecylglycine	Ncdec
15	D- ² -methylvaline	Dmval	N-cyclododecylglycine	Ncdod
	D-N-methylalanine	Dnmala	N-cyclooctylglycine	Ncoct
	D-N-methylarginine	Dnmarg	N-cyclopropylglycine	Nopro
	D-N-methyleasparagine	Dnmasn	N-cycloundecylglycine	Ncund
	D-N-methyleaspartate	Dnmasp	N-(2,2-diphenylethyl)glycine	Nbhm
20	D-N-methylcysteine	Dnmcys	N-(3,3-diphenylpropyl)glycine	Nbhe
	D-N-methylglutamine	Dnmgln	N-(3-guanidinopropyl)glycine	Narg
	D-N-methylglutamate	Dnmglu	N-(1-hydroxyethyl)glycine	Nthr
	D-N-methylhistidine	Dnmhis	N-(hydroxyethyl)glycine	Nser
	D-N-methylisoleucine	Dnmile	N-(imidazolylethyl)glycine	Nhis
25	D-N-methylelleucine	Dnmleu	N-(3-indolylyethyl)glycine	Nhtrp
	D-N-methyllysine	Dnmlys	N-methyl-(-aminobutyrate	Nmgabu
	N-methylcyclohexylalanine	Nmchexa	D-N-methylmethionine	Dnmmet
	D-N-methylornithine	Dnmorn	N-methylcyclopentylalanine	
	NmcpenN-methylglycine	Nala	D-N-methylphenylalanine	Dnmphe
30	N-methylaminoisobutyrate	Nmaib	D-N-methylproline	Dnmpro
	N-(1-methylpropyl)glycine	Nile	D-N-methylserine	Dnmser
	N-(2-methylpropyl)glycine	Nieu	D-N-methylthreonine	Dnmthr
	D-N-methyltryptophan	Dnmtrp	N-(1-methylethyl)glycine	Nval
	D-N-methyltyrosine	Dnmtyr	N-methyla-naphylalanine	Nmanap
35	D-N-methylvaline	Dnmval	N-methylpenicillamine	Nmpen
	(-aminobutyric acid	Gabu	N-(p-hydroxyphenyl)glycine	Nhtyr
	L-t-butylglycine	Tbug	N-(thiomethyl)glycine	Ncys

	L-ethylglycine	Etg	penicillamine	Pen
	L-homophenylalanine	Hphe	L--methylalanine	Mala
	L--methylarginine	Marg	L--methylasparagine	Masn
	L--methylaspartate	Masp	L--methyl-t-butylglycine	Mtbug
5	L--methylcysteine	Mcys	L-methylethylglycine	Metg
	L--methylglutamine	Mgln	L--methylglutamate	Mglu
	L--methylhistidine	Mhis	L--methylhomophenylalanine	Mhphe
	L--methylisoleucine	Mile	N-(2-methylthioethyl)glycine	Nmet
	L--methylleucine	Mleu	L--methyllysine	Mlys
10	L--methylmethionine	Mmet	L--methylnorleucine	Mnle
	L--methylnorvaline	Mnva	L--methylornithine	Morn
	L--methylphenylalanine	Mphe	L--methylproline	Mpro
	L--methylserine	Mser	L--methylthreonine	Mthr
	L--methyltryptophan	Mtrp	L--methyltyrosine	Mtyr
15	L--methylvaline	Mval	L-N-methylhomophenylalanine	Nmhphe
	N-(N-(2,2-diphenylethyl) carbamylmethyl)glycine	Nnbhm	N-(N-(3,3-diphenylpropyl) carbamylmethyl)glycine	Nnbhe
	1-carboxy-1-(2,2-diphenyl- Nmhc		ethylamino)cyclopropane	

20

The present invention further contemplates chemical analogues of NR6 capable of acting as antagonists or agonists of NR6 or which can act as functional analogues of NR6. Chemical analogues may not necessarily be derived from NR6 but may share certain conformational similarities. Alternatively, chemical analogues may be specifically designed to mimic certain physicochemical properties of NR6. Chemical analogues may be chemically synthesised or may be detected following, for example, natural product screening.

The identification of NR6 permits the generation of a range of therapeutic molecules capable of modulating expression of NR6 or modulating the activity of NR6. Modulators contemplated by the present invention includes agonists and antagonists of NR6 expression. Antagonists of NR6 expression include antisense

molecules, ribozymes and co-suppression molecules. Agonists include molecules which increase promoter ability or interfere with negative regulatory mechanisms. Agonists of NR6 include molecules which 5 overcome any negative regulatory mechanism. Antagonists of NR6 include antibodies and inhibitor peptide fragments.

Other derivatives contemplated by the present invention 10 include a range of glycosylation variants from a completely unglycosylated molecule to a modified glycosylated molecule. Altered glycosylation patterns may result from expression of recombinant molecules in different host cells.

15 Another embodiment of the present invention contemplates a method for modulating expression of NR6 in a subject such as a human or mouse, said method comprising contacting the genetic sequence encoding NR6 with an effective amount of a modulator of NR6 20 expression for a time and under conditions sufficient to up-regulate or down-regulate or otherwise modulate expression of NR6. Modulating NR6 expression provides a means of modulating NR6-ligand interaction or NR6 25 stimulation of cell activities.

Another aspect of the present invention contemplates a 30 method of modulating activity of NR6 in a human, said method comprising administering to said mammal a modulating effective amount of a molecule for a time and under conditions sufficient to increase or decrease NR6 activity. The molecule may be a proteinaceous molecule or a chemical entity and may also be a derivative of NR6 or its ligand or a chemical analogue or truncation 35 mutant of NR6 or its ligand.

The present invention, therefore, contemplates a

pharmaceutical composition comprising NR6 or a derivative thereof or a modulator of NR6 expression or NR6 activity and one or more pharmaceutically acceptable carriers and/or diluents. These components are referred to as the Active ingredients@.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions (where water soluble) and sterile powders for the extemporaneous preparation of sterile injectable solutions. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dilution medium comprising, for example, water, ethanol, polyol (for example, glycerol, propylene glycol and liquid polyethylene glycol, and the like), suitable mixtures thereof, and vegetable oils. The proper fluidity can be maintained, for example, by the use of surfactants. The preventions of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions are prepared by incorporating the active compounds in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilization. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and the freeze-drying

technique which yield a powder of the active ingredient plus any additional desired ingredient from previously sterile-filtered solution thereof.

5 When the active ingredients are suitably protected they may be orally administered, for example, with an inert diluent or with an assimilable edible carrier, or it may be enclosed in hard or soft shell gelatin capsule, or it may be compressed into tablets, or it may be
10 incorporated directly with the food of the diet. For oral therapeutic administration, the active compound may be incorporated with excipients and used in the form of ingestible tablets, buccal tablets, troches, capsules, elixirs, suspensions, syrups, wafers, and the like.
15 Such compositions and preparations should contain at least 1% by weight of active compound. The percentage of the compositions and preparations may, of course, be varied and may conveniently be between about 5 to about 80% of the weight of the unit. The amount of active
20 compound in such therapeutically useful compositions is such that a suitable dosage will be obtained. Preferred compositions or preparations according to the present invention are prepared so that an oral dosage unit form contains between about 0.1 ug and 2000 mg of active
25 compound. Alternative dosage amounts include from about 1 Fg to about 1000 mg and from about 10 Fg to about 500 mg.

30 The tablets, troches, pills, capsules and the like may also contain the components as listed hereafter: A binder such as gum, acacia, corn starch or gelatin; excipients such as dicalcium phosphate; a disintegrating agent such as corn starch, potato starch, alginic acid and the like; a lubricant such as
35 magnesium stearate; and a sweetening agent such as sucrose, lactose or saccharin may be added or a flavouring agent such as peppermint, oil of wintergreen,

or cherry flavouring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar or both. A syrup or elixir may contain the active compound, sucrose as a sweetening agent, methyl and propylparabens as preservatives, a dye and flavouring such as cherry or orange flavour. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compound(s) may be incorporated into sustained-release preparations and formulations.

The present invention also extends to forms suitable for topical application such as creams, lotions and gels as well as a range of "paints" which are applied to skin and through which the active ingredients are absorbed.

Pharmaceutically acceptable carriers and/or diluents include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutical active substances is well known in the art and except insofar as any conventional media or agent is incompatible with the active ingredient, their use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units

suited as unitary dosages for the mammalian subjects to be treated; each unit containing a predetermined quantity of active material calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the novel dosage unit forms of the invention are dictated by and directly dependent on (a) the unique characteristics of the active material and the particular therapeutic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active material for the treatment of disease in living subjects having a diseased condition in which bodily health is impaired as herein disclosed in detail.

The principal active ingredient is compounded for convenient and effective administration in effective amounts with a suitable pharmaceutically acceptable carrier in dosage unit form as hereinbefore disclosed. A unit dosage form can, for example, contain the principal active compound in amounts ranging from 0.5 :g to about 2000 mg. Expressed in proportions, the active compound is generally present in from about 0.5 :g to about 2000 mg/ml of carrier. In the case of compositions containing supplementary active ingredients, the dosages are determined by reference to the usual dose and manner of administration of the said ingredients.

Dosages may also be expressed per body weight of the recipient. For example, from about 10 ng to about 1000 mg/kg body weight, from about 100 ng to about 500 mg/kg body weight and for about 1 Fg to above 250 mg/kg body weight may be administered.

The pharmaceutical composition may also comprise genetic molecules such as a vector capable of transfecting target cells where the vector carries a nucleic acid molecule capable of modulating NR6 expression or NR6

activity. The vector may, for example, be a viral vector.

Still another aspect of the present invention is directed to antibodies to NR6 and its derivatives. Such antibodies may be monoclonal or polyclonal and may be selected from naturally occurring antibodies to NR6 or may be specifically raised to NR6 or derivatives thereof. In the case of the latter, NR6 or its derivatives may first need to be associated with a carrier molecule. The antibodies and/or recombinant NR6 or its derivatives of the present invention are particularly useful as therapeutic or diagnostic agents. For example, NR6 antibodies or antibodies to its ligand may act as antagonists.

For example, NR6 and its derivatives can be used to screen for naturally occurring antibodies to NR6. These may occur, for example in some autoimmune diseases. Alternatively, specific antibodies can be used to screen for NR6. Techniques for such assays are well known in the art and include, for example, sandwich assays and ELISA. Knowledge of NR6 levels may be important for diagnosis of certain cancers or a predisposition to cancers or for monitoring certain therapeutic protocols.

Antibodies to NR6 of the present invention may be monoclonal or polyclonal. Alternatively, fragments of antibodies may be used such as Fab fragments. Furthermore, the present invention extends to recombinant and synthetic antibodies and to antibody hybrids. A "synthetic antibody" is considered herein to include fragments and hybrids of antibodies. The antibodies of this aspect of the present invention are particularly useful for immunotherapy and may also be used as a diagnostic tool for assessing apoptosis or monitoring the program of a therapeutic regimen.

For example, specific antibodies can be used to screen for NR6 proteins. The latter would be important, for example, as a means for screening for levels of NR6 in a cell extract or other biological fluid or purifying NR6 made by recombinant means from culture supernatant fluid. Techniques for the assays contemplated herein are known in the art and include, for example, sandwich assays and ELISA.

It is within the scope of this invention to include any second antibodies (monoclonal, polyclonal or fragments of antibodies or synthetic antibodies) directed to the first mentioned antibodies discussed above. Both the first and second antibodies may be used in detection assays or a first antibody may be used with a commercially available anti-immunoglobulin antibody. An antibody as contemplated herein includes any antibody specific to any region of NR6.

Both polyclonal and monoclonal antibodies are obtainable by immunization with the enzyme or protein and either type is utilizable for immunoassays. The methods of obtaining both types of sera are well known in the art. Polyclonal sera are less preferred but are relatively easily prepared by injection of a suitable laboratory animal with an effective amount of NR6, or antigenic parts thereof, collecting serum from the animal, and isolating specific sera by any of the known immunoabsorbent techniques. Although antibodies produced by this method are utilizable in virtually any type of immunoassay, they are generally less favoured because of the potential heterogeneity of the product.

The use of monoclonal antibodies in an immunoassay is particularly preferred because of the ability to produce them in large quantities and the homogeneity of the product. The preparation of hybridoma cell lines for

monoclonal antibody production derived by fusing an immortal cell line and lymphocytes sensitized against the immunogenic preparation can be done by techniques which are well known to those who are skilled in the art.

Another aspect of the present invention contemplates a method for detecting NR6 in a biological sample from a subject said method comprising contacting said 10 biological sample with an antibody specific for NR6 or its derivatives or homologues for a time and under conditions sufficient for an antibody-NR6 complex to form, and then detecting said complex.

The presence of NR6 may be accomplished in a number of ways such as by Western blotting and ELISA procedures. 15 A wide range of immunoassay techniques are available as can be seen by reference to US Patent Nos. 4,016,043, 4, 424,279 and 4,018,653. These, of course, includes both single-site and two-site or "sandwich" assays of the 20 non-competitive types, as well as in the traditional competitive binding assays. These assays also include direct binding of a labelled antibody to a target.

Sandwich assays are among the most useful and commonly 25 used assays and are favoured for use in the present invention. A number of variations of the sandwich assay technique exist, and all are intended to be encompassed by the present invention. Briefly, in a typical forward assay, an unlabelled antibody is immobilized on a solid 30 substrate and the sample to be tested brought into contact with the bound molecule. After a suitable period of incubation, for a period of time sufficient to allow formation of an antibody-antigen complex, a second antibody specific to the antigen, labelled with a 35 reporter molecule capable of producing a detectable signal is then added and incubated, allowing time sufficient for the formation of another complex of

antibody-antigen-labelled antibody. Any unreacted material is washed away, and the presence of the antigen is determined by observation of a signal produced by the reporter molecule. The results may either be
5 qualitative, by simple observation of the visible signal, or may be quantitated by comparing with a control sample containing known amounts of hapten.
Variations on the forward assay include a simultaneous assay, in which both sample and labelled antibody are
10 added simultaneously to the bound antibody. These techniques are well known to those skilled in the art, including any minor variations as will be readily apparent. In accordance with the present invention, the sample is one which might contain NR6 including cell
15 extract, tissue biopsy or possibly serum, saliva, mucosal secretions, lymph, tissue fluid and respiratory fluid. The sample is, therefore, generally a biological sample comprising biological fluid but also extends to fermentation fluid and supernatant fluid such as from a
20 cell culture.

In the typical forward sandwich assay, a first antibody having specificity for the NR6 or antigenic parts thereof, is either covalently or passively bound to a solid surface. The solid surface is typically glass or
25 a polymer, the most commonly used polymers being cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene. The solid supports may be in the form of tubes, beads, discs of microplates, or any
30 other surface suitable for conducting an immunoassay. The binding processes are well-known in the art and generally consist of cross-linking covalently binding or physically adsorbing, the polymer-antibody complex is washed in preparation for the test sample. An aliquot
35 of the sample to be tested is then added to the solid phase complex and incubated for a period of time sufficient (e.g. 2-40 minutes or overnight if more

convenient) and under suitable conditions (e.g. from about room temperature to about 37°C) to allow binding of any subunit present in the antibody. Following the incubation period, the antibody subunit solid phase is washed and dried and incubated with a second antibody specific for a portion of the hapten. The second antibody is linked to a reporter molecule which is used to indicate the binding of the second antibody to the hapten.

An alternative method involves immobilizing the target molecules in the biological sample and then exposing the immobilized target to specific antibody which may or may not be labelled with a reporter molecule. Depending on the amount of target and the strength of the reporter molecule signal, a bound target may be detectable by direct labelling with the antibody. Alternatively, a second labelled antibody, specific to the first antibody is exposed to the target-first antibody complex to form a target-first antibody-second antibody tertiary complex. The complex is detected by the signal emitted by the reporter molecule.

In another alternative method, the NR6 ligand is immobilised to a solid support and a biological sample containing NR6 brought into contact with its immobilised ligand. Binding between NR5 and its ligand can then be determined using an antibody to NR6 which itself may be labelled with a reporter molecule or a further anti-immunoglobulin antibody labelled with a reporter molecule could be used to detect antibody bound to NR6.

By "reporter molecule" as used in the present specification, is meant a molecule which, by its chemical nature, provides an analytically identifiable signal which allows the detection of antigen-bound antibody. Detection may be either qualitative or

quantitative. The most commonly used reporter molecules in this type of assay are either enzymes, fluorophores or radionuclide containing molecules (i.e. radioisotopes) and chemiluminescent molecules.

5 In the case of an enzyme immunoassay, an enzyme is conjugated to the second antibody, generally by means of glutaraldehyde or periodate. As will be readily recognized, however, a wide variety of different conjugation techniques exist, which are readily available to the skilled artisan. Commonly used enzymes include horseradish peroxidase, glucose oxidase, beta-galactosidase and alkaline phosphatase, amongst others.

10 The substrates to be used with the specific enzymes are generally chosen for the production, upon hydrolysis by the corresponding enzyme, of a detectable colour change.

15 Examples of suitable enzymes include alkaline phosphatase and peroxidase. It is also possible to employ fluorogenic substrates, which yield a fluorescent product rather than the chromogenic substrates noted above.

20 In all cases, the enzyme-labelled antibody is added to the first antibody hapten complex, allowed to bind, and then the excess reagent is washed away. A solution containing the appropriate substrate is then added to the complex of antibody-antigen-antibody. The substrate will react with the enzyme linked to the

25 second antibody, giving a qualitative visual signal, which may be further quantitated, usually spectrophotometrically, to give an indication of the amount of hapten which was present in the sample.

30 "Reporter molecule" also extends to use of cell agglutination or inhibition of agglutination such as red blood cells on latex beads, and the like.

35 Alternately, fluorescent compounds, such as fluorescein and rhodamine, may be chemically coupled to antibodies without altering their binding capacity. When activated by illumination with light of a particular wavelength,

the fluorochrome-labelled antibody adsorbs the light energy, inducing a state to excitability in the molecule, followed by emission of the light at a characteristic colour visually detectable with a light microscope. As in the EIA, the fluorescent labelled antibody is allowed to bind to the first antibody-hapten complex. After washing off the unbound reagent, the remaining tertiary complex is then exposed to the light of the appropriate wavelength the fluorescence observed indicates the presence of the hapten of interest.

Immunofluorescence and EIA techniques are both very well established in the art and are particularly preferred for the present method. However, other reporter molecules, such as radioisotope, chemiluminescent or bioluminescent molecules, may also be employed.

The present invention also contemplates genetic assays such as involving PCR analysis to detect the NR6 gene or its derivatives. Alternative methods or methods used in conjunction include direct nucleotide sequencing or mutation scanning such as single stranded conformational polymorphisms analysis (SSCP) as specific oligonucleotide hybridisation, as methods such as direct protein truncation tests.

The nucleic acid molecules of the present invention may be DNA or RNA. When the nucleic acid molecule is in a DNA form, it may be genomic DNA or cDNA. RNA forms of the nucleic acid molecules of the present invention are generally mRNA.

Although the nucleic acid molecules of the present invention are generally in isolated form, they may be integrated into or ligated to or otherwise fused or associated with other genetic molecules such as vector molecules and in particular expression vector molecules. Vectors and expression vectors are generally capable of

replication and, if applicable, expression in one or both of a prokaryotic cell or a eukaryotic cell. Preferably, prokaryotic cells include *E. coli*, *Bacillus sp* and *Pseudomonas sp*. Preferred eukaryotic cells 5 include yeast, fungal, mammalian and insect cells.

Accordingly, another aspect of the present invention contemplates a genetic construct comprising a vector portion and a mammalian and more particularly a human 10 NR6 gene portion, which NR6 gene portion is capable of encoding an NR6 polypeptide or a functional or immunologically interactive derivative thereof.

Preferably, the NR6 gene portion of the genetic 15 construct is operably linked to a promoter on the vector such that said promoter is capable of directing expression of said NR6 gene portion in an appropriate cell.

20 In addition, the NR6 gene portion of the genetic construct may comprise all or part of the gene fused to another genetic sequence such as a nucleotide sequence encoding maltose binding protein or glutathione-S-transferase or part thereof.

25 The present invention extends to such genetic constructs and to prokaryotic or eukaryotic cells comprising same.

30 The present invention also extends to any or all derivatives of NR6 including mutants, part, fragments, portions, homologues and analogues or their encoding 35 genetic sequence including single or multiple nucleotide or amino acid substitutions, additions and/or deletions to the naturally occurring nucleotide or amino acid sequence.

NR6 may be important for the proliferation,

differentiation and survival of a diverse array of cell types. Accordingly, it is proposed that NR6 or its functional derivatives be used to regulate development, maintenance or regeneration in an array of different cells and tissues *in vitro* and *in vivo*. For example, 5 NR6 is contemplated to be useful in modulating neuronal proliferation, differentiation and survival.

Soluble NR6 polypeptides are also contemplated to be 10 useful in the treatment of a range of diseases, injuries or abnormalities.

Membrane bound or soluble NR6 may be used *in vitro* on nerve cells or tissues to modulate proliferation, 15 differentiation or survival, for example, in grafting procedures or transplantation.

As stated above, the NR6 of the present invention or its functional derivatives may be provided in a 20 pharmaceutical composition comprising the NR6 together with one or more pharmaceutically acceptable carriers and/or diluents. In addition, the present invention contemplates a method of treatment comprising the administration of an effective amount of a NR6 of the 25 present invention. The present invention also extends to antagonists and agonists of NR6s and their use in therapeutic compositions and methodologies.

A further aspect of the present invention contemplates 30 the use of NR6 or its functional derivatives in the manufacture of a medicament for the treatment of NR6 mediated conditions defective or deficient.

Still a further aspect of the present invention 35 contemplates a ligand for NR6 preferably, in isolated or recombinant form or a derivative of said ligand.

The present invention further contemplates knockout animals such as mice or other murine species for the NR6 gene including homozygous and heterozygous knockout animals. Such animals provide a particularly useful live in vivo model for studying the effects of NR6 as well as screening for agents capable of acting as agonists or antagonists of NR6.

According to this embodiment there is provided a transgenic animal comprising a mutation in at least one allele of the gene encoding NR6. Additionally, the present invention provides a transgenic animal comprising a mutation in two alleles of the gene encoding NR6. Preferably, the transgenic animal is a murine animal such as a mouse or rat.

The present invention is further described by the following non-limiting Figures and Examples.

In the Figures:

Figure 1 is a diagrammatic representation showing expansion of sequenced region of the mouse NR6 gene indicating splicing patterns seen in the three forms of NR6 cDNA, NR6.1, NR6.2 and NR6.3.

Figure 2 is a representation of the nucleotide sequence of the mouse NR6 gene, containing exons encoding the cDNA from nucleotide 148 encoding D50 of the cDNAs shown in SEQ ID NOS:12 and 14 to the end of the 3N untranslated region shared by both NR6.1, NR6.2 and NR6.3. In this figure, this region encompasses nucleotides g1182 to g6617. This sequence is also defined in SEQ ID NO:28.

Figure 3 is a representation of the nucleotide sequence of the mouse genomic NR6 gene with additional 5N

sequences. The coding exons of NR6 span approximately 11kb of the mouse genome. There are 9 coding exons separated by 8 introns:

	exon1	at least 239nt	intron1 5195nt
5	exon 2	282nt	intron2 214nt
	exon3	130nt	intron3 107nt
	exon4	170nt	intron4 1372nt
	exon5	158nt	intron5 68nt
	exon6	169nt	intron6 2020nt
10	exon6	188nt	intron7 104nt
	exon8	43nt	intron8 181nt
	exon9	252nt	

Exon 1 encoding the signal sequence, exon 2 the Ig-like domain, exons 3 to 6 the hemopoietin domain. Exons 7, 8 and 9 are alternatively spliced.

Figure 4 is a diagrammatic representation showing the genomic structure of murine NR-6.

20

Figure 5 is a diagrammatic representation showing targetting of the NR6 locus by homologous recombination.

Single and three letter abbreviations for amino acid residues used in the specification are summarised in Table 2:

5

TABLE 2

	Amino Acid	Three-letter Abbreviation	One-letter Symbol
10	Alanine	Ala	A
	Arginine	Arg	R
	Asparagine	Asn	N
	Aspartic acid	Asp	D
	Cysteine	Cys	C
15	Glutamine	Gln	Q
	Glutamic acid	Glu	E
	Glycine	Gly	G
	Histidine	His	H
	Isoleucine	Ile	I
20	Leucine	Leu	L
	Lysine	Lys	K
	Methionine	Met	M
	Phenylalanine	Phe	F
	Proline	Pro	P
25	Serine	Ser	S
	Threonine	Thr	T
	Tryptophan	Trp	W
	Tyrosine	Tyr	Y
	Valine	Val	V
30	Any residue	Xaa	X

TABLE 3
SUMMARY OF SEQ ID NO.

	Sequence	SEQ ID NO.
5	Amino acid sequence WSXWS	1
	Oligonucleotide primers and probes listed in Example 1	2-11
	Nucleotide sequence of NR6.1 ¹	12
	Amino acid sequence of NR6.1	13
10	Nucleotide sequence of NR6.2 ²	14
	Amino acid sequence of NR6.2	15
	Nucleotide sequence of NR6.3 ³	16
	Amino acid sequence of NR6.3	17
	Nucleotide sequence of products generated by 5N RACE of brain cDNA using NR6 specific primers ⁴	18
	Amino acid sequence of SEQ ID NO:18	19
	Nucleotide sequence unique to 5N RACE of brain cDNA	20
20	Amino acid sequence for SEQ ID NO:20	21
	Unspliced murine NR6 nucleotide sequence	22
	PCR product for human NR6	23
	Nucleotide sequence of clone HFK-66 encoding human NR6	24
25	Amino acid sequence of SEQ ID NO:24	25
	Oligonucleotide sequences UP1 and LP1, respectively	26-27
	Genomic nucleotide sequence of murine NR6	28
	Amino acid sequence of SEQ ID NO:28	29
30	Murine NR6.1 oligonucleotide primers	30, 31
	Murine IL-3 signal sequence	32
	Linker sequence for mouse IL-3 signal sequence and FLAG epitope	33-35
	Genomic nucleotide sequence of murine NR6 containing additonal 5N sequence	38
35	Oligonucleotide 2199 and 2200, respectively	36, 37
	N-terminal region of NR6	39

¹The polyadenylation signal AATAAAATAAA is at nucleotide position 1451 to 1460; NR6.1 (SEQ ID NO:12) and NR6.2 (SEQ ID NO:14) are identical to nucleotide 1223 encoding Q407, the represents the end of an exon. NR6.1 splices out an exon present only in NR6.2 and uses a different reading frame for the final exon which is shared with NR6.2; this corresponds to amino acids VLPAKL at amino acid residue positions 408-413. The region of 3N-untranslated DNA shared by NR6.1, NR6.2 and NR6.3 is from nucleotide 1240 to 1475. The WSXWS motif is at amino acid residues 330 to 334.

²The polyadenylation signal AATAAA is at nucleotide positions 1494 to 1503. The WSXWS motif is at amino acid residues 330 to 334. NR6.1 and NR6.2 are identical to nucleotide 1223 encoding Q407 which represents the end of an exon. NR6.2 splices in an exon beginning at amino acid residue D408, nucleotide 1224 and ends at residue G422, nucleotide 1264. The region of 3N untranslated DNA shared by NR6.1, NR6.2 and NR6.3 is from nucleotide position 1283 to 1517.

³The nucleotide and amino acid numbering corresponds to SEQ ID NO:12 and 14. The WSXWS motif is at amino acid residues 330 to 334. The polyadenylation signal AATAAAATAAA is from nucleotide 1781 to 1780. NR6.1, NR6.2 and NR6.3 are identical to nucleotide 1223 encoding Q407, this represents the end of an exon. NR6.3 fails to splice from this position and, therefore, translation continues through the intron, giving rise to the C-terminal protein region from amino acid residues 408 to 461. The region of 3N untranslated DNA shared by NR6.1, NR6.2 and NR6.3 is from nucleotide 1469 to 1804.

³⁵⁴The nucleotide sequence is identical to NR6.1, NR6.2 and NR6.3 from nucleotide C151, the first nucleotide for Pro51. The numbering from this nucleotide is the same

as for SEQ ID NO:14 and 16. The 5N of this point is unique to the products generated by 5N RACE not being found in NR6.1, NR6.2 and NR6.3 and is represented in SEQ ID NOS:20 and 21.

5

⁵Structure of the murine genomic NR6 locus. The coding exons of NR6 span approximately 11kb of the mouse genome. There are 9 coding exons separated by 8 introns:

10

	exon 1 at least 239nt	introns1 5195nt
	exon 2 282nt	introns2 214nt
	exon 3 130nt	introns3 107nt
	exon 4 170nt	introns4 1372nt
15	exon 5 158nt	introns5 68nt
	exon 6 169nt	introns6 2020nt
	exon 7 188nt	introns7 104nt
	exon 8 43nt	introns8 181nt
	exon 9 252nt	

20

Exon 1 encodes the signal sequence, exon 2 the Ig-like domain, exons 3 to 6 the hemopoietin domain. Exons 7, 8 and 9 are alternatively spliced.

25 The NRG molecules of the present invention have a range of utilities referred to in the subject specification. Additional utilities include:

30 1. Identification of molecules that interact with NR6. These may include :

- a) a corresponding ligand using standard orphan receptor techniques (26),
- 35 b) monoclonal antibodies that act either as receptors antagonists or agonists,

c) mimetic or antagonistic peptides isolated using phage display technology (27, 28),

5 d) small molecule natural products that act either as antagonists or agonists.

2. Development of diagnostics to detect deletions/rearrangements in the NR6 gene.

10 The NR6 knock-out mice studies described herein provide a useful model for this utility. There are also applications in the field of reproduction. For example, people can be tested for their NR6 status. NR6 +/- carriers might be expected to give rise to offspring with developmental problems.

EXAMPLE 1

Oligonucleotides

	M116:	5' ACTCGCTCCAGATTCCCGCCTTT 3'	[SEQ ID NO:2]
5	M108:	5' TCCCGCCTTTTCGACCCATAGAT 3'	[SEQ ID NO:3]
	M159:	5' GGTACTTGGCTTGAAAGAGGAAAT 3'	[SEQ ID NO:4]
	M242:	5' CGGCTCACGTGCACGTCGGGTGGG 3'	[SEQ ID NO:5]
	M112:	5' AGCTGCTGTTAAAGGGCTTCTC 3'	[SEQ ID NO:6]
	WSDWS	5' (A/G) CTCCA (A/G) TC (A/G) CTCCA 3'	[SEQ ID NO:7]
10	WSEWS	5' (A/G) CTCCA (C/T) TC (A/G) CTCCA 3'	[SEQ ID NO:8]
	1944	5' AAGTGTGACCATCATGTGGAC 3'	[SEQ ID NO:9]
	2106	5' GGAGGTGTTAAGGAGGCG 3'	[SEQ ID NO:10]
	2120	5' ATGCCCGCGGGTCGCCCG 3'	[SEQ ID NO:11]

15 EXAMPLE 2

Isolation of initial NR6 cDNA clones using oligonucleotides designed against the conserved WSXWS motif found in members of the haemopoietin receptor family

20
(i) A commercial adult mouse testis cDNA library cloned
into the UNI-ZAP bacteriophage (Stratagene, CA, USA;
Catalogue numbers 937 308) was used to infect
Escherichia coli of the strain LE392. Infected bacteria
25 were grown on twenty 150 mm agar plates, to give
approximately 50,000 plaques per plate. Plaques were
then transferred to duplicate 150 mm diameter nylon
membranes (Colony/Plaque Screen, NEN Research Products,
MA, USA), bacteria were lysed and the DNA was denatured
30 and fixed by autoclaving at 100°C for 1 min with dry
exhaust. The filters were rinsed twice in 0.1% (w/v)
sodium dodecyl sulfate (SDS), 0.1 x SSC (SSC is 150 mM
sodium chloride, 15 mM sodium citrate dihydrate) at room
temperature and pre-hybridized overnight at 42°C in 6 x
35 SSC containing 2 mg/ml bovine serum albumin, 2 mg/ml
Ficoll, 2 mg/ml polyvinylpyrrolidone, 100 mM ATP, 10
mg/ml tRNA, 2 mM sodium pyrophosphate, 2 mg/ml salmon

sperm DNA, 0.1% (w/v) SDS and 200 mg/ml sodium azide. The pre-hybridisation buffer was removed. 1.2 Fg of the degenerate oligonucleotides for hybridization (WSDWS; Example 1) were phosphorylated with T4 polynucleotide kinase using 960 mCi of $\gamma^{32}\text{P}$ -ATP (Bresatec, S.A., Australia). Unincorporated ATP was separated from the labelled oligonucleotide using a pre-packed gel filtration column (NAP-5; Pharmacia, Uppsala, Sweden). Filters were hybridized overnight at 42°C in 80 ml of the prehybridisation buffer containing 0.1% (w/v) SDS, rather than NP40, and 10^6 - 10^7 cpm/ml of labelled oligonucleotide. Filters were briefly rinsed twice at room temperature in 6 x SSC, 0.1% (v/v) SDS, twice for 30 min at 45°C in a shaking waterbath containing 1.5 l of the same buffer and then briefly in 6 x SSC at room temperature. Filters were then blotted dry and exposed to autoradiographic film at -70°C using intensifying screens, for 7 - 14 days prior to development.

Plaques that appeared positive on orientated duplicate filters were picked, eluted in 1 ml of 100 mM NaCl, 10 mM MgCl₂, 10 mM Tris.HCl pH7.4 containing 0.5% (w/v) gelatin and 0.5% (v/v) chloroform and stored at 4°C. After 2 days LE392 cells were infected with the eluate from the primary plugs and replated for the secondary screen. This process was repeated until hybridizing plaques were pure.

Once purified, positive cDNAs were excised from the ZAP II bacteriophage according to the manufacturer's instructions (Stratagene, CA, USA) and cloned into the plasmid pBluescript. A CsCl purified preparation of the DNA was made and this was sequenced on both strands. Sequencing was performed using an Applied Biosystems automated DNA sequencer, with fluorescent dideoxynucleotide analogues according to the manufacturer's instructions. The DNA sequence was analysed using software supplied by Applied Biosystems.

Two clones isolated from the mouse testis cDNA library shared large regions of nucleotide sequence identity 68-1 and 68-2 and appeared to encode a novel member of the haemopoietin receptor family and the inventors gave the putative receptor the working name "NR6".
5

(ii) In a parallel series of experiments, a commercial mouse brain cDNA library (STRATAGENE #967319, Balb/c day-20, whole brain cDNA/Uni-ZAP XR Vector) was used to
10 infect *E.coli* strain XL1-Blue MRF=. Infected bacteria were grown on 90x135mm square agar plates to give about 25,000 plaques per plate. Plaques were then transferred to positively charged nylon membranes, Hybond-N(+) (Amersham RPN 203B), bacteria were lysed and the DNA was
15 denatured with denaturing 0.5 M NaOH, 1.5 M NaCl at room temperature for 7 min. The membranes were neutralized with 0.5 M Tris-HCL pH7.2, 1.5 M NaCl, 1 mM EDTA at room temperature for 10 min before the DNA fixation by UV crosslinking.
20

A mixture of WSDWS and WSEWS oligonucleotide probes (SEQ ID NOS: 7 and 8) were labelled with a $[{}^32\text{P}]$ -ATP (TOYOBIO #PNK-104 Kination kit). The membranes from the mouse brain cDNA library were then hybridized with the
25 mixture of WSDWS and WSEWS oligonucleotide probes in the Rapid Hybridization Buffer (Amersham, RPN1636) at 42°C for 16 hours. Filters were washed with 1xSSC/0.1% (w/v) SDS at 42°C before autoradiography. Plaques that appeared positive on orientated duplicate filters were
30 picked and replated on *E. coli*, XL1-Blue MRFN with the process of immobilisation on nylon membranes, hybridization of membranes with oligonucleotide probes, washing and autoradiography repeated until pure plaques had been obtained.
35

The cDNA fragment from pure positively hybridizing plaques was isolated by excision with the helper phage

strain ExAssist according to the manufacturer=s instructions (Stratagene, #967319). Sequencing was performed after the amplification with Ampli-Taq DNA polymerase and Taq dideoxy terminator cycle sequencing kit (Perkin Elmer, #401150) by 25 cycles of 96°C for 10 sec, 50°C for 5 sec, 60°C for 4 min followed by 60°C for 5 min with the sequencing primers on an ABI model 377 DNA sequencer.

One clone, MBC-8, from the mouse brain library shared large regions of nucleotide sequence identity with both the 68-1 and 68-2 clones isolated from the mouse testis cDNA library.

(iii) In a third series of experiments, total RNA was prepared from the mouse osteoblastic cell line, KUSA, according to the method of Chirgwin et al. (15), and poly(A)+RNA was further purified by oligo(dT)-cellulose chromatography (Pharmacia Biotech). Complementary DNA was synthesized by oligo(dT) priming, inserted into the UniZAP XR directional cloning vector (Stratagene), and packaged into 8 phage using Gigapack Gold (Stratagene), yielding 1.25×10^7 independent clones.

Approximately 10^6 clones were screened essentially as described in (ii) above. Briefly, probes were labeled with ^{32}P using T4 polynucleotide kinase and prehybridization was performed for 4 hr in the Rapid hybridization buffer (Amersham LIFE SCIENCE) at 42°C. Filters (Hybond N+, Amersham) were then hybridized for 19 hr under the same condition with the addition of ^{32}P -labeled WSXWS mix oligonucleotides and washed 3 times. The final wash was for 30 min in 1 x SSPE, 0.1% (w/v) SDS at 42°C. Filters were then exposed with an intensifying screen to Kodak X-OMAT AR film for 5 days.

Isolated clones were subjected to the *in vivo* excision

of pBluescript SK(-) phagemid (Stratagene), and plasmid DNA was prepared by the standard method. DNA sequences were determined using an ABI PRISM 377 DNA Sequencer (Perkin Elmer) with appropriate synthetic oligonucleotide primers. A clone pKUSA166 shared large regions of nucleotide sequence identity with the MBC-8, 68-1 and 68-2 clones isolated from the mouse brain and testis cDNA libraries.

10

EXAMPLE 3

Isolation of further NR6 cDNA clones using probes specific for NR6

(i) In order to identify other cDNA libraries containing cDNA clones for NR6, the inventors performed PCR upon 1 µl aliquots of λ-bacteriophage cDNA libraries made from mRNA from various human tissues and using oligonucleotides 2070 and 2057, designed from the sequence of 68-1 and 68-2, as primers. Reactions contained 5 µl of 10 x concentrated PCR buffer (Boehringer Mannheim GmbH, Mannheim, Germany), 1 µl of 10 mM dATP, dCTP, dGTP and dTTP, 2.5 µl of the oligonucleotides HYB2 and either T3 or T7 at a concentration of 100 mg/ml, 0.5 µl of Taq polymerase (Boehringer Mannheim GmbH) and water to a final volume of 50 µl. PCR was carried out in a Perkin-Elmer 9600 by heating the reactions to 96°C for 2 min and then for 25 cycles at 96°C for 30 sec, 55°C for 30 sec and 72°C for 2 min. PCR products were resolved on an agarose gel, immobilized on a nylon membrane and hybridized with ³²P-labelled oligonucleotide 1943 (SEQ ID NO:42).

In addition to the original library, a mouse brain cDNA library appeared to contain NR6 cDNAs. These were screened using a ³²P-labelled oligonucleotides 1944, 2106, 2120 (Example 1) or with a fragment of the original NR6 cDNA clone from 68-1 (nucleotide 934 to the

end of NR6.1 in Figure 1) labelled with ^{32}P using a random decanucleotide labelling kit (Bresatec). Conditions used were similar to those described in (i) above except that for the labelled oligonucleotides, 5 filters were washed at 55°C rather than 45°C, while for the NR6 cDNA fragment prehybridization and hybridization was carried out in 2xSSC and filters were washed at 0.2 x SSC at 65°C. Again, as described in (i) above, positively hybridising plaques were purified, the cDNAs 10 were recovered and cloned into plasmids pBluescript II or pUC19. Independent cDNA clones were sequenced on both strands.

15 Using this procedure, 6 further clones, 68-5, 68-35, 68-41, 68-51, 68-77 and 73-23, contained large regions of sequence identity with 68-1, 68-2, MBC-8 and pKUSA166.

In a parallel series of experiments, further screening 20 was performed with hybridization probes prepared from the 1.7 kbp EcoRI-XhoI fragment excised from pKUSA166. This fragment was excised and labeled with ^{32}P by using T7QuickPrime Kit (Pharmacia Biotech). Approximately 25 6×10^5 clones were screened. Hybond N+ filters (Amersham) were first prehybridized for 4hr at 42°C in 50% (v/v) formamide, 5xSSPE, 5xDenhardt's solution, 0.1% 30 (w/v) SDS, and 0.1mg/ml denatured salmon sperm DNA. Hybridization was for 16 hours under the same conditions with the addition of ^{32}P - labelled NR6- cDNA fragment 35 probes. Finally the filters were washed once for 1hr in 0.2xSSC, 0.1% (w/v) SDS at 68°C. Eight clones were isolated, and phage clones were subjected to the *in vivo* excision of the pBluescript SK(-) phagemid (Stratagene). The plasmid DNAs were prepared by the standard method. DNA sequences were determined by an ABI PRISM 377 DNA Sequencer using appropriate synthetic oligonucleotide primers.

Using this procedure 8 further clones from the KUSA library contained large regions of sequence identity with 68-1, 68-2, MBC-8, pKUSA166, 68-5, 68-35, 68-41, 68-51, 68-77 and 73-23 were isolated.

5

EXAMPLE 4**Isolation of genomic DNA encoding NR6**

DNA encoding the murine NR6 genomic locus was also isolated using the 68-1 cDNA as a probe. Two positive clones, 2-2 and 57-3, were isolated from a mouse 129/Sv strain genomic DNA library cloned into λ FIX. These clones were overlapping and the position of the restriction sites, introns and exons were determined in the conventional manner. The region of the genomic clones containing exons and the intervening introns were sequenced on both strands using an Applied Biosystems automated DNA sequencer, with fluorescent dideoxynucleotide analogues according to the manufacturer's instructions. Figure 2 shows the nucleotide sequence and corresponding amino acid sequence of the translation regions. This is also shown in SEQ ID NOS:30 and 31. Figure 3 provides the genomic NR6 gene sequence but with additional 5N sequence. This is also represented in SEQ ID NO:38 in relation to this sequence. The coding exons of NR6 span approximately 11kb of the mouse genome. There are 9 coding exons separated by 8 introns:

30	exon1	at least 239nt	intron1	5195nt
	exon2	282nt	intron2	214nt
	exon3	130nt	intron3	107nt
	exon4	170nt	intron4	1372nt
	exon5	158nt	intron5	68nt
35	exon6	169nt	intron6	2020nt
	exon7	188nt	intron7	104nt
	exon8	43nt	intron8	181nt

exon9 252nt

Exon 1 encodes the signal sequence, exon 2 the Ig-like domain, exons 3 to 6 the hemopoietin domain. Exons 7, 8 and 9 are alternatively spliced.

EXAMPLE 5
10 SN RACE analysis of NR6

5'-RACE was used to investigate the nature of the sequence 5' of nucleotide 960, encoding Ile321 of NR6.1, 2 and 3. The nucleotide and corresponding amino acid sequences are shown in SEQ ID NOs:12, 14 and 16, respectively. 5'-RACE was performed using Advantage KlenTaq polymerase (CLONTECH, CAT NO. K1905-1) on mouse brain Marathon-ready cDNA (CLONTECH, CAT NO. 7450-1) according to the manufacturer's instructions. Briefly, the first rounds of amplification were performed using 5 μ l of cDNA in a total volume of 50 μ l, with 1mM each of the primers AP1&M116 [SEQ ID NO:2] or AP1&M159 [SEQ ID NO:4] by 35 cycles of 94°C x 0.5min, 68°C x 2.0min on GeneAmp 2400 (Perkin-Elmer). An amount of 5 μ l of 50-fold diluted product from the first amplification was then re-amplified ; for the products generated with primers AP1 and M116 [SEQ ID NO:2] in the first amplification, 1 mM of the primers AP2&M108 [SEQ ID NO:3] were used in the second amplification. For the products generated with primers AP1 and M116 [SEQ ID NO:2] in the first amplification, two separate secondary reactions were performed, one reaction with 1 mM primers AP2&M242 [SEQ ID NO:5] and the other with 1 mM primers AP2&M112 [SEQ ID NO:6]. Amplification was achieved using 25 cycles of 94°C x 0.5min, 68°C x 2.0min. These samples were analyzed by agarose gel electrophoresis. When a single ethidium bromide staining amplification

product was observed, it was purified by QIAquick PCR purification kit according to the manufacturer=s instructions (QIAGEN, CAT NO. DG-0281) and its sequence was directly determined using both primers used in the secondary amplification step, that is AP2 and either M108 [SEQ ID NO:3], M242 [SEQ ID NO:5] or M112 [SEQ ID NO:6].

EXAMPLE 6

10

Cloning of NR6

From the initial screens of mouse brain and testis cDNA libraries with the degenerate WSXWS oligonucleotides and subsequent screening of cDNA libraries from mouse testis, mouse brain and the KUSA osteoblastic cells line a total of 18 NR6 cDNAs have been isolated. Nucleotide sequence of NR6 was also determined from 5'RACE analysis of brain cDNA. Additionally, two murine genomic DNA clones encoding NR6 have also been isolated.

20

Comparison of the NR6 cDNA clones revealed a common region of nucleotide sequence which included a 123 base pairs 5'-untranslated region and 1221 base pairs open reading frame, stretching from the putative initiation methionine, Met1 to Gln407 (SEQ ID NOs:12, 14 and 16, respectively). Within this common open reading frame, a haemopoietin receptor domain was observed which contained the four conserved cysteine residues and the five amino acid motif WSXWS typical of members of the haemopoietin receptor family, was observed.

30
Further analyses revealed that after nucleotide 1221, three different classes of NR6 cDNAs could be found, these were termed NR6.1, NR6.2 and NR6.3 (SEQ ID NOs:12, 14 and 16, respectively). Each encoded a receptor that appeared to lack a classical transmembrane domain and, would, therefore be likely to be secreted into the

extracellular environment. Although the putative C-terminal region of the three classes of NR6 proteins appear to be different, the cDNAs encoding them also had a common region of 3'-untranslated region.

5

With regard to SEQ ID NOs:12, 14 and 16, the number of both nucleotides and amino acids begins at the putative initiation methione. NR6.1 and NR6.2 are identical to nucleotide 1223 encoding Q407, this represents the end 10 of an exon. NR6.1 splices out an exon present only in NR6.2 and uses a different reading frame for the final exon which is shared with NR6.2. The 3N-untranslated region is shared by NR6.1, NR6.2 and NR6.3, NR6.2 splices in an exon starting with nucleotide 1224 15 encoding D408 and ending with nucleotide 1264 encoding the first nucleotide in the codon for G422 and uses a different reading frame for the final exon which is shared with NR6.2 (see Figure 1). NR6.3 fails to splice from position nucleotide 1224, therefore, translation 20 continues through the intron, giving rise to the C-terminal protein region.

The sequence of NR6 cDNA products generated by 5'-RACE amplification from mouse brain cDNA preparation is 25 shown in SEQ ID NO:18. The nucleotide sequence identified using 5'-RACE appeared to be identical to the sequence of cDNAs encoding NR6.1, NR6.2, and NR6.3 from nucleotide C151, the first nucleotide for the codon for Pro51. 5' of this nucleotide, the sequences diverged 30 and the sequence is unique not being found in NR6.1, NR6.2 or NR6.3. Additionally, there is a single nucleotide difference, with the sequence from the RACE containing an G rather than an A at nucleotide 475, resulting in Thr159 becoming Ala.

35

Analysis of the genomic clones, revealed that they were overlapping and contained exons encoding the majority of

the coding region of the three forms of NR6 (Figures 1, 2 and 3). These genomic clones, contained exons encoding from Asp50 (nucleotide 148) of the NR6 cDNAs. Sequence 5' of this in the cDNAs, including the 5'-untranslated region and the region encoding Met1 to Gln49 (SEQ ID NOs:12, 14 and 16), and the 5' end predicted from analysis of 5' RACE products (SEQ ID NO:18) were not present in the two genomic clones isolated.

10

Analysis of the NR6 genomic DNA clones also provided an explanation of the three classes of NR6 cDNAs found. It is likely that NR6.1, NR6.2 and NR6.3 arise through alternative splicing of NR6 mRNA (Figure 1). The last amino acid residue that these different NR6 proteins are predicted to share is Gln407. SEQ ID NO:18 shows that Gln407 is the last amino acid encoded by the exon that covers nucleotides g5850 to g6037 (see Figure 2). Alternative splicing from the end of this exon (Figure 1) accounts for the generation of cDNAs encoding NR6.1 (SEQ ID NO:12), NR6.2 (SEQ ID NO:14) and NR6.3 (SEQ ID NO:16). In the case of NR6.1, the region from g6038 to g6425 is spliced out, leading to juxtaposition of g6037 and g6426. In the case of NR6.2, the region from g6038 to 6141 is spliced out, an exon from 6142 to g6183 is retained and then this is followed by splicing out of the region from g6183 to g6425. NR6.3 appears to arise when there is no splicing from nucleotide g6038. For all three forms, a secreted rather than transmembrane form is generated, these differ however in their predicted C-terminal region. The genomic NR6 sequence with additional 5N sequence is shown in Figure 3.

35

EXAMPLE 7
ESTs

Databases were searched with the murine NR6

corresponding to the unspliced version shown in SEQ ID NO:16. The murine NR6 sequence used is shown in SEQ ID NO:22.

The databases searched were:

5

(i) dbEST - Database of Expressed Sequence Tags
National Center for Biotechnology Information National
Library of Medicine, 38A, 8N8058600 Rockville Pike,
Bethesda, MD 20894 Phone: 0011-1-301-496-2475 Fax:
10 0015-1-301-480-9241 USA.

(ii) DNA Data Bank of Japan DNA Database Release 3689.
Prepared by: Sanzo Miyazawa Manager/Database
Administrator Hidenori Hayashida Scientific Reviewer
15 Yukiko Yamazaki/Eriko Hatada/Hiroaki Serizawa
Annotators/reviewers Motono Horie/Shigeko Suzuki/Yumiko
Satao Secretaries/typists DNA Data Bank of Japan National
Institute of Genetics Center for Genetic Information
research Laboratory of Genetic Information Analyses 1111
20 Yata Mishima, Shizuoka 411 Japan.

25

(iii) EMBL Nucleic Acid Sequence Data Bank Release
47.0.

25

(iv) EMBL Nucleic Acid Sequence Data Bank Weekly Updates
Since Release 44.

30

(v) Genetic Sequence Data Bank NCBI-GenBank Release 94
National Center for Biotechnology Information National
Library of Medicine, 38A, 8N805 8600 Rockville Pike,
Bethesda, MD 20894 Phone: 0011-1-301-495-2475 Fax:
0015-1-301-480-9241 USA.

35

(vi) Cumulative Updates since NCBI-GenBank Release 88
National Center for Biotechnology Information National
Library of Medicine, 38A, 8N805 8600 Rockville Pike,
Bethesda, MD 20894 USA.

The search of the databases with the murine probe identified several EST's having sequence similarity to the probe. The EST's were:

- 5 W66776 (murine sequence)
 MM5839 (murine sequence)
 AA014965 (murine sequence)
 W46604 (human sequence)
 W46603 (human sequence)
10 H14009 (human sequence)
 N78873 (human sequence)
 R87407 (human sequence) .

EXAMPLE 8

15 Isolation of 3N cDNA clones encoding human NR6

PCR products encoding human NR6 were generated using oligonucleotides UP1 and LP1 (see below) based on human ESTs (Genbank Acc:H14009, Genbank Acc:AA042914) that 20 were identified from databases searched with murine NR6 sequence (SEQ ID NO:22). PCR was performed on a human fetal liver cDNA library (Marathon ready cDNA CLONTECH #7403-1) using Advantage Klen Taq Polymerase mix (CLONTECH #8417-1) in the buffer supplied at 94°C fro 25 30s and 68°C for 3 min for 35 cycles followed by 68°C for 4 min and then stopping at 15°C. A standard PCR programme for the Perkin-Elmer GeneAmp PCT system 2400 thermal cycle was used. The PCR yielded a prominent product of approximately 560 base pairs (bp; SEQ ID NO:18), which was radiolabelled with $[{}^{-32}P]$ dCTP using a 30 random priming method (Amersham, RPN, 1607, Mega prime kit) and used to screen a human fetal kidney 5N-STRETCH PLUS cDNA library (CLONTECH #HL1150x). Library screens were performed using Rapid Hybridisation Buffer 35 (Amersham, RPN 1636) according to manufacturer's instructions and membranes washed at 65°C for 30 min in 0.1xSSC/0.1% (w/v) SDS. Two independent cDNA clones

were obtained as lambda phage and subsequently subcloned and sequenced. Both clones (HFK-63 and HFK-66) contained 1.4 kilobase (kb) inserts that showed sequence similarity with murine NR6. The sequence and 5 corresponding amino acid translation of HFK-66 is shown in SEQ ID NO:24.

The translation protein sequences of clone HFK-66 shows a high degree of sequence similarity with the mouse NR6.

10

OLIGONUCLEOTIDES

UP1: 5NTCC AGG CAG CGG TCG GGG GAC AAC 3N [SEQ ID NO:26]

LP1: 5N TTG CTC ACA TCG TCC ACC ACC TTC 3N [SEQ ID
NO:27]

15

EXAMPLE 9

Genomic Structure of Human NR6

Human genomic DNA clones encoding human NR6 was 20 isolated by screening a human genomic library (Lambda FIXJII Stratagene 946203) with radiolabelled oligonucleotides, 2199 and 2200 (see below). These oligonucleotides were designed based on human ESTs (Genbank Acc:R87407, Genbank Acc:H14009) that were 25 identified from databases searched with murine NR6. Filters were hybridised overnight at 37°C in 6xSSC containing 2 mg/ml bovine serum albumin, 2 mg/ml Ficoll, 2mg/ml polyvinylpyrrolidone, 100 mM ATP, 10 mg/ml tRNA, 2 mM sodium pyrophosphate, 2 mg/ml salmon sperm DNA, 30 0.1% (w/v) SDS and 200 mg/ml sodium azide and washed at 65°C in 6 x SSC/0.1% SDS. Five independent genomic clones were obtained and sequenced. The extend of sequence obtained has determined that the clones overlap and exhibit a similar genomic structure to murine NR6. 35 Exon coding regions are almost identical over the region covered by the genomic clones while intron coding regions differ, although the size of the introns are

comparable. The extent of known overlap is shown in Fig. 5.

OLIGONUCLEOTIDES:

5

2199: 5N CCC ACG CTT CTC ATC GGA TTC TCC CTG 3N [SEQ ID NO:36]

2200: 5N CAG TCC ACA CTG TCC TCC ACT CGG TAG 3N [SEQ ID NO:37]

10

EXAMPLE 10

Northern Blot Analysis of Human NR6 mRNA Expression

15 Clontech Multiple Tissue Northern Blots (Human MTN Blot, CLONTECH #7760-1, Human MTN Blot IV, CLONTECH #7766-I, Human Brain MTN Blot II, CLONTECH #7755-1, Human Brain MTN Blot III, CLONTECH #7750) were probed with a radiolabelled 3N human NR6 cDNA clone, HFK-66 (SEQ ID NO:24). The clone was labelled with [³²P] dCTP using a 20 random priming method (Amersham, RPN 1607, Mega prime kit). Hybridisation was performed in Express Hybridisation Solution (CLONTECH H50910) for 3 hours at 67°C and membranes were washed in 0.1xSSC/0.1% w/v SDS 25 at 50°C.

A 1.8 kb transcript was detected in a variety of human tissues encompassing reproductive, digestive and neural tissues. High levels were observed in the heart, 30 placenta, skeletal muscle, prostate and various areas of the brain, lower levels were observed in the testis, uterus, small intestine and colon. Photographs showing these Northern blots are available upon request. This expression pattern differs from the expression pattern 35 observed with murine NR6.

EXAMPLE 11

- 53 -

Mouse NR6 Expression Vectors

pEF-FLAG/mNR6.1

5 The mature coding region of mouse NR6.1 was amplified using the PCR to introduce an in-frame *Asc* I restriction enzyme site at the 5' end of the mature coding region and an *Mlu* I site at the 3' end, using the following oligonucleotides:-

10 5N oligo 5N-AGCTGGCGCGCCTCCGGGCGGATCGGGAGCCCAC-3N [SEQ ID NO:30]
3N oligo 5N-AGCTACGCGTTAGAGTTAGCCGGCAG-3N [SEQ ID NO:31]

15 The resulting PCR derived DNA fragment was then digested with *Asc* I and *Mlu* I and cloned into the *Mlu* I site of pEF-FLAG. Expression of NR6 is under the control of the polypeptide chain elongation factor 1 α promoter as described (16) and results in the secretion, using the IL3 signal sequence from pEF-FLAG, of N-terminal FLAG-tagged NR6 protein.

20 25 pEF-FLAG was generated by modifying the expression vector pEF-BOS as follows:-

30 pEF-BOS (16) was digested with *Xba* I and a linker was synthesized that encoded the mouse IL3 signal sequence (MVLASSTTSIHTMLLLLLMLFHLGLQASIS) and the FLAG epitope (DYKDDDDK). *Asc* I and *Mlu* I restriction enzyme sites were also introduced as cloning sites. The sequence of the linker is as follows:-

35 M V L A S S T T S I H T
M
CTAGACTAGTGCTGACACAATGGTTCTGCCAGCTCTACCACCAGCATCCACACCA
TG

TGATCACGACTGTGTTACCAAGAACGGTCGAGATGGTGGTCGTAGGTGTGGTAC

L L L L M L F H L G L Q A S I S Asc
5 I
CTGCTCCTGCTCCTGATGCTCTTCCACCTGGACTCCAAGCTTCAATCTCGGCGCG
CC
GACGAGGACGAGGACTAGCAGAAGGTGGACCCTGAGGTTCGAAGTTAGAGCCGCGC
GG
10 D Y K D D D D K Mlu I
AGGACTACAAGGACGACGATGACAAGACGCGTGCTAGCACTAGT

TCCTGATGTTCTGCTGCTACTGTTCTGCGCACGATCGTATCAGATC

15 The two oligonucleotides were annealed together and
ligated into the Xba I site of pEF-BOS to give pEF-FLAG.

pCOS1/FLAG/mNR6 & pCHO1/FLAG/mNR6

20 A DNA fragment containing the sequences encoding IL3
signal sequence/Flag/mNR6 and the poly(A) adenylation
signal from human G-CSF cDNA, was excised from pEF-
FLAG/mNR6 using the restriction enzyme EcoR I. This DNA
25 fragment was then inserted into the EcoR I cloning site
of pCOS1 and pCHO1

The pCOS1 and pCHO1 vectors were constructed as follows.
pCHO1 is also described in reference (17) but with a
30 different selectable marker.

pCOS1 was prepared by digesting HEF-12h-g"1 (see Figure
24 of International Patent Publication No. WO 92/19759)
with EcoRI and SmaI and ligating the digesting product
35 with an EcoRI-NotI-BamHI adaptor (Takara 4510). The
resulting plasmid comprises an EFI" promoter/enhancer,
Nco^r marker gene, SV40E, ori and an Amp^r marker gene.

pCH01 was constructed by digesting DHFR-PMh-grl (see Figure 25 of International Patent Publication No. WO 92/19759) with *Pvu*I and *Eco*47III and ligating same with pCOSI digested with *Pvu*I and *Eco*47III. The resulting vector, pCH01, comprises an EFI" promoter/enhancer, an DHFR marker gene, SV40E, Ori and a Amp^r gene.

EXAMPLE 12

10

mRN6 has been expressed as an NN Flag tagged protein following transfection of CHO cells and as a CN Flag tagged protein following transfection of KUSA cells in both cases varying levels of dimeric and aggregated NR6 were secreted.

15

EXAMPLE 13

Murine NR6 expression

20

NR6 expression studies were conducted in murine Northern Blots. At the level of sensitivity used in the adult mouse, NR6 expression was detected in salivary gland, lung and testis. During embryonic development, NR6 is expressed in fetal tissues from day 10 of gestation through to birth. In cell lines, NR6 expression has been observed in the T-lymphoid line CTLL-2 as well as in FD-PyMT (FDC-P1 myeloid cells expressing polyoma midle T gene), and fibroblastoid cells including bone marrow and fetal liver stromal lines.

30

EXAMPLE 14

Expression, purification and characterisation of CHO and KUSA mNR6

35

The methods provide for the production of a dimeric form of CHO derived NN FLAG-mNR6 without refolding. All

other methods are capable of producing NR6 and are encompassed by the present invention.

5 A. Production of CHO derived N' FLAG-mNR6 (dimeric form)

(i) Protein Production

To analyse structure and functional activity, a cDNA fragment containing the entire coding sequence of murine NR6 with an N-terminal FLAG (NN FLAG) sequence was 10 cloned into the EcoR1 site of the expression vector pCHO1. For stable production of N-terminal FLAG-tagged NR6 the vector contains the DHFR (dihydrofolate 15 reductase) gene as a selective marker with the NR6 gene under the control of an EF1 α promoter. CHO cells were transfected with the construct using a polycationic 20 liposome transfection reagent (Lipofectamine, GibcoBRL).

(ii) Lipofectamine transfection method

20 Using six well tissue culture plates either 2×10^5 KUSA cells in 2ml IMDM + 10% (v/v) FCS or 2×10^5 CHO cells were cultured in 2ml "-MEM + 10% (v/v) FCS until 70% confluent. 2Fg DNA diluted in 100Fl OPTI-MEM I (Gibco BRL, USA) was mixed gently with 12Fl lipofectamine diluted in 100Fl OPTI-MEM I and incubated at room temperature for 30min to allow DNA complex formation. DNA complexes were gently diluted in a total volume of 1ml of OPTI-MEM I and overlaid onto washed KUSA or CHO 25 cell monolayers. A further 1ml IMDM + 20% (v/v) FCS (KUSA cells) or 1ml "-MEM + 20% (v/v) FCS (CHO cells) was added to transfected cells after 5 hours. At 24 hours, the culture medium was replaced with fresh complete growth medium. At 48 hours after transfection, 30 selection was applied. A methotrexate resistant clone secreting comparatively high levels of NR6 was selected and expanded for further analysis.

(iii) Protein expression

CHO cells were grown to confluence in roller bottles in nucleoside free "-MEM + 10% (v/v) FCS. Selection was maintained by using 100 ng/ml Methotrexate in the conditioned media according to manufacturer instructions. Expression was monitored by Biosensor and harvesting found to be optimal at 3 to 4 days.

10 B. Protein Analysis

(i) Biosensor analysis

Expression and purification was monitored by Biosensor analysis (BiaCoreTM, Sweden) where anti FLAG peptide M2 antibody (Kodak Eastman, USA), specific for the FLAG peptide sequence was bound to the sensorchip. Fractions were analysed for binding to the sensor surface (resonance units) and the sample then removed from the surface using 50 mM Diethylamine pH 12.0 prior to analysis of the next fraction. Immobilisation and running conditions of the Biosensor follow the manufacturer's instructions.

25 (ii) Protein Production

In order to generate and characterise NR6, conditioned media (2 L) produced by CHO cells was harvested after day 3, post confluence. Conditioned media was concentrated using diafiltration with a 10,000 molecular weight cut-off. (Easy flow, Sartorius, Aus). At a volume of 200 ml (i.e. 10 x concentrated) the sample was buffer exchanged into 20 mM Tris, 0.15M NaCl, 0.02% (v/v) Tween 20 pH 7.5 (Buffer A).

35

(iii) Immunoprecipitation and Western Blot analysis of mNR6

Concentrated conditioned media (1ml) was immunoprecipitated with M2 affinity resin (20F1, Kodak Eastman). To examine the structural characterisation of mNR6 SDS PAGE was performed under reducing and non-reducing conditions. Separation was performed on NOVEX 4-20% (v/v) Tris/glycine gradient gels and protein transferred on PVDF membrane. Western blots were probed with biotinylated M2 antibody (primary, 1:500) and then streptavidin peroxidase (secondary, 1:3000). Samples were visualised by autoradiography using electrochemiluminescence (ECL, Dupont, USA).

By regressive analysis of prestained standards (BIORAD, Aus.) the molecular weight of the monomeric unit was calculated to be 65,000 daltons. Under non-reducing conditions the molecular weight was calculated to be 127,000 indicating that NR6 is a disulphide linked dimer. A tetrameric complex running at approximately 250,000 daltons was also observed. Although a band running at approximately 50,000 daltons was observed, no monomeric NR6 was detected under non-reducing conditions indicating that the majority of NR6 expressed in this system is disulphide linked.

25 (iv) Affinity Chromatography of mNR6

Concentrated conditioned media (200 ml) was applied to M2 affinity resin (5ml) under gravity. To enhance recovery the unbound fraction was reapplied to the column four times prior to extensive washing of the column with 200 volumes of Buffer A. Biosensor analysis indicates that approximately 20% of the M2 binding originally present in the concentrate remains in the unbound fraction. The bound fraction was eluted from the column using an immunodesorbant (50 ml); actisep (Sterogene Labs, USA).

(v) Ion exchange and Desalting of mNR6

In order to buffer exchange mNR6 prior to anion chromatography, 10 ml batches of the eluted fraction (50 ml) were applied to an XK column (400 x 26 mm I.D.) containing G25 sepharose (Pharmacia, Sweden).
5 Chromatography was developed at 4 ml/min using an FPLC (Pharmacia, Sweden) equipped with an online UV280 and conductivity monitor. The mobile phase was 10 mM Tris, 10 0.1M NaCl, 0.02% v/v Tween, pH 8.0. 10 ml fractions were collected between 12.5 min and 25 min to optimise recovery and removal of salt. Fractions were analysed by Biosensor analysis and pooled according to binding.

15 All pooled active fractions were diluted with an equal volume of 20 mM Tris, 0.02% (v/v) Tween, pH 8.5 (Buffer B) and then loaded onto a Mono Q 5/5 (Pharmacia, Sweden) at a flow rate of 2 ml/min. The column was washed with buffer B. Elution was performed using a linear gradient 20 between buffer B and buffer B containing 0.6M NaCl over 30 min at a flow rate of 1 ml/min. Fractions (1 minute) were collected and analysed on the Biosensor and also by SDS PAGE and Western blot analysis. Fractions 15 to 26 (approximately 0.4M NaCl) appear to contain the majority 25 of mNR6 as indicated by the Biosensor.

C. Production of CHO derived N' FLAG-mNR6 (monomeric form)

30 (i) Protein Production

A cDNA fragment containing the entire coding sequence of murine NR6 with an N-terminal FLAGJ sequence was cloned 35 into the expression vector pCHO1 for production of N-terminal FLAG-tagged protein. This vector contains a neomycin resistance gene with expression of the NR6 gene under the control of an EF1" promoter. This expression

construct was transfected into CHO cells using Lipofectamine (Gibco BRL, USA) according to the manufacturer instructions. Transfected cells were cultured in IMDM + 10% (v/v) FCS with resistant cells selected in geneticin (600Fg/ml, Gibco BRL, USA). A neomycin resistant clone, secreting comparatively high levels of NR6 was selected and expanded for further analysis.

10 (ii) Protein expression

N' FLAG-NR6 expressed in serum free conditioned media (10 litre) was harvested from transfected CHO and cells. Collected media was concentrated using a CH2 ultrafiltration system equipped with a S1Y10 cartridge (Amicon molecular weight cut-off 10,000). Preliminary examination of the expressed product under reducing and non-reducing SDS PAGE followed by western blot analysis was performed. Visualisation of the protein on Westerns was specific to the primary antibody anti FLAG M2. Under reducing conditions a band approximately at 65,000 daltons was observed. Under non-reducing conditions, dimer and larger molecular weight aggregates were observed. These are disulphide linked monomers as they are not present in the reducing gel. Small amounts of monomer appear to be present in non-reducing gels.

25 (iii) Affinity Chromatography of NR6

Concentrated conditioned media was applied to an anti FLAG M2 affinity resin (100 x 16 mm I.D.). After washing the unbound proteins off the column, the bound proteins were eluted using FLAG peptide (60Fg/ml) in PBS.

30 (iv) Ion Exchange Chromatography of NR6

35 Eluted fractions from affinity column were dialysed overnight against 20 mM Tris-HCl pH 8.5 (buffer C)

containing 50 mM Dithiothreitol (DTT) using 25,000 cut-off dialysis tubing (Spectra/Por7, Spectrum). The dialysed fractions were loaded onto Mono Q 5/5 (Pharmacia, Sweden) previously equilibrated with buffer C containing 5 mM DTT. Chromatography was developed using a linear gradient between buffer C and buffer C containing 1.0 M NaCl at a flow rate of 0.5 ml / min.

5 (v) Refolding of NR6

10

Fractions containing NR6 from the Mono Q were adjusted to 50 mM DTT and left overnight at 41C. To initiated refolding the sample was then dialysed against 50 mM Tris-HCl (pH 8.5), 2 M Urea, 0.1% (v/v) Tween 20, 10 mM Glutathione (reduced) and 2 mM Glutathione (oxidised) at a final protein concentration of 100 Fg / ml. Folding was carried out at ambient temperature with one change of the buffer over 24 hours.

15 20 (v) Reversed Phase High Performance Liquid Chromatography (RP-HPLC)

The folded product was further purified by RP-HPLC using a Vydac C4 resin (250 x 4.6 mm I.D.) previously equilibrated with 0.1% (v/v) Trifluoroacetic acid (TFA). Elution was carried out using a linear gradient from 0 to 80% (v/v) acetonitrile / 0.1% (v/v) TFA at a flow rate of 1 ml per minute.

25 30 D. pCHO1/NR6/FLAG

In order to determine the native N termini of NR6, a C terminal FLAG NR6 CHO cell line was established.

35 The plasmid pKUSA166 (murine NR6 cDNA cloned into the EcoR I site of pBLUESCRIPT) was digested with BamH I to remove the sequences encoding the last 15 amino acids of murine NR6. Synthetic oligonucleotides which encode the

3' end of mouse NR6 followed by the FLAG peptide tag were annealed and ligated into the BamH I site of pKUSA166. The sequence of the oligonucleotides was as follows:-

5

I L P S G R R G A A R G P A G D Y K D
D D D K * [SEQ ID NO:34]
GATCTTGCCTCGGGCAGACGGGGTGCAGCGAGAGGTCCCTGCCGGCGACTACAAGG
10 ACGACGATGACAAGTA G [SEQ ID NO:33]
AACGGGAGCCCGTCTGCCACGCCGCTCTCCAGGACGGCCGCTGATGTTCCCTGCT
GCTACTGTTCATCCTAG [SEQ ID NO:35]

The 5' end of the linker introduces a silent mutation (CTG > TTG), to destroy the 5' BamH I site upon insertion of the linker. The NR6 cDNA (with native signal sequence) with the C-terminal FLAG was cut out of pKUSA166 with EcoR I and BamH I and cloned into the EcoR I - BamH I cloning sites of pCHO-1. This vector results in the secretion of NR6 protein with a C-terminal flag tag (CN FLAG-mRN6).

This vector results in the secretion of NR6 protein from KUSA cells. The vector pCHO1 has been previously described in (17) although with a different secretable marker.

(i) Production of polyclonal NR6 antiserum
30 The following peptide from the N terminal area of NR6 was chosen for production of polyclonal antiserum to NR6

VISPPQDPPTLLIGSSLQATCSIHGDT [SEQ ID NO:39]

35 The peptide was conjugated to KLH and injected into rabbits. Production and purification of the polyclonal antibody specific to the NR6 peptide sequence follows

standard methods.

(ii) Protein expression

5 KUSA cells transfected with cDNA of C terminal tagged mNR6 were grown to confluence in flasks (800ml) using IMDM media containing 10% (v/v) FBS. Conditioned media (100 ml) was harvested 3 -4 days post confluence.

10 (iii) Characterisation of NR6 by Immunoprecipitation and Western blotting

In order to establish that NR6 with the predicted sequence is produced in KUSA cells transfected with the 15 cDNA, western blot analysis using both M2 antibody and purified NR6 specific rabbit antibody were performed. Conditioned media (1 to 5 ml) was immunoprecipitated with M2 affinity resin (10-20 F1). Then after sufficient time for binding, the beads were washed with MT-PBS and subsequently NR6 eluted with 100 Fg/ml FLAG peptide (40 F1, (1, 5 minute incubation)). The sample was then 20 subjected to reducing and non reducing SDS PAGE followed by western blot analysis. Both purified NR6 polyclonal antibody (purified by protein G) and M2 antibody 25 recognise a band under reducing conditions of a molecular weight size approximately 65,000 daltons. Since the two antibodies reconising resides at the N terminus and C terminus it is reasonable to assume that full length NR6 is produced. Biotinylation of the 30 respective antibodies by standard methods reduces the background. Under non-reducing conditions polyclonal NR6 bind antibodies to a band of a molecular weight of approximately 127,000, consistent with a dimeric NR6 disulphide linked form. Minor components of tetrameric 35 NR6 are present, no monomeric NR6 is evident using polyclonal NR6 antibodies.

EXAMPLE 15
Generation of NR6 knockout mice

To construct the NR6 targeting vector, 4.1kb of genomic
5 NR6 DNA containing exons 2 through to 6 was deleted and
replaced with G418-resistance cassette, leaving 5N and
3N NR6 arms of 2.9 and 4.5 kb respectively. A 4.5 kb
Xhol fragment of the murine genomic NR6 clone 2.2
(Figure 3) containing exons 7, 8 and 3N flanking
10 sequence was subcloned into the Xhol site of pBluescript
generating pBSNR6Xho4.5. A 2.9kb NotI-StuI fragment
within NR6 intron 1 from the same genomic clone was
inserted into NotI and EcoRV digested pBSNR6Xho4.5
creating pNR6-Ex2-6. This plasmid was digested with
15 Clal, which was situated between the two NR6 fragments,
and following blunt ending, ligated with a blunted 6kb
HindIII fragment from placZneo, which contains the
lacZgene and a PGKneo cassette, to generate the final
targeting vector, pNR6lacZneo. pNR6lacZneo was
20 linearised with NotI and electroporated into W9.5
embryonic stem cells. After 48 hours, transfected cells
were selected in 175 Fg/ml G418 and resistant clones
picked and expanded after a further 8 days.

25 Clones in which the targetting vector had recombined
with the endogenous NR6 gene were identified by
hybridising SpeI-digested genomic DNA with a 0.6 kb
XhoI-StuI fragment from genomic NR6 clone 2.2. This
probe (probe A, Figure 4), which is located 3N to the
30 NR6 sequences in the targeting vector, distinguished
between the endogenous (9.9 kb) and targeted (7.1 kb)
NR6 loci (Figure 5).

Genomic DNA was digested with SpeI for 16hrs at 371C,
35 electrophoresed through 0.8% (w/v) agarose, transferred
to nylon membranes and hybridised to ³²P-labelled probe
in a solution containing 0.5M sodium phosphate, 7% (w/v)

SDS, 1mM EDTA and washed in a solution containing 40mM sodium phosphate, 1% (w/v) SDS at 65°C. Hybridising bands were visualised by autoradiography for 16 hours at -70°C using Kodak XAR-5 film and intensifying screens.

5 Two targeted ES cell clones, W9.5NR6-2-44 and W9.5NR6-4-2, were injected into C57Bl/6 blastocysts to generate chimeric mice. Male chimeras were mated with C57Bl/6 females to yield NR6 heterozygotes which were subsequently interbred to produce wild-type (NR6^{+/+}), 10 heterozygous (NR6^{+/-}) and mutant (NR6^{-/-}) mice. The genotypes of offspring were determined by Southern Blot analysis of genomic DNA extracted from tail biopsies.

15 Genotyping of mice at weaning from matings between NR^{+/-} heterozygous mice derived from both targated ES cell clones revealed an absence of homozygous NR6^{-/-} mutants. As no unusual loss of mice was observed between birth and weaning, this suggest that lack of NR6 is lethal during embryonic development or immediately after birth. 20 Genotyping of embryonic tissues at various stages of development suggests that death occurs late in gestation (beyond day 16) or at birth.

EXAMPLE 16

25 Oligonucleotides

1943:

5' GTC CAA GTG CGT TGT AAC CCA 3'

2070:

5' GCT GAG TGT GCG CTG GGT CTC ACC 3'

30 2057:

5' GGC TCC ACT CGC TCC AGA 3'

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications. The

invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of said steps or features.

5

BIBLIOGRAPHY:

1. Du, X.X. and Williams, D.A. (1994) *Blood* 83: 2023-2030.
- 5 2. Yang, Y.C. and Yin, T. (1992) *Biofactors* 4: 15-21.
3. Paul, S.R., Bennett, F., Calvetti, J.A., Kelleher, K., Wood, C.R., O'Hara, R.J.J., Leary, A.C., Sibley, B., Clark, S.C., Williams, D.A. and Yang, Y.-C. (1990) *Proc. Natl. Acad. Sci. USA* 87: 7512.
- 10 4. Musashi, M., Clark, S.C., Sudo, T., Urdal, D.L., and Ogawa, M. (1991) *Blood* 78: 1448-1451.
5. Schibler, K.R., Yang, Y.C. and Christensen, R.D. (1992) *Blood* 80: 900-3.
- 15 6. Tsuji, K., Lyman, S.D., Sudo, T., Clark, S.C., and Ogawa, M. (1992) *Blood* 79: 2855-60.
7. Burstein, S.A., Mei, R.L., Henthorn, J., Friese, P. and Turner, K. (1992) *J. Cell. Physiol.* 153: 305-12.
- 20 8. Hangoc, G., Yin, T., Cooper, S., Schendel, P., Yang, Y.C. and Broxmeyer, H.E. (1993) *Blood* 81: 965-72.
9. Teramura, M., Kobayashi, S., Hoshino, S., Oshimi, K. and Mizoguchi, H. (1992) *Blood* 79: 327-31.
- 25 10. Yonemura, Y., Kawakita, M., Masuda, T., Fujimoto, K., Kato, K. and Takatsuki, K. (1992) *Exp. Hematol.* 20: 1011-6.
11. Baumann, H. and Schendel, P. (1991) *J. Biol. Chem.* 266: 20424-7.
- 30 12. Kawashima, I., Ohsumi, J., Mita-Honjo, K., Shimoda-Takano, K., Ishikawa, H., Sakakibara, S., Miyadai, K. and Takiguchi, Y. (1991) *Febs. Lett.* 283: 199-202.
13. Keller, D.C., Du, X.X., Srour, E.F., Hoffman, R. and Williams, D.A. (1993) *Blood* 82: 1428-35.
- 35 14. Sambrook et al (1989) *Cloning: A Laboratory Manual*. Cold Spring Harbour Laboratory, Cold Spring

- Harbour, NY.
15. Chirgwin et al (1979) *Biochemistry* 18: 5294-5299.
16. Mizushima and Nagata (1990) *Nucl. Acids Res.*, 18: 5322.
- 5 17. *FEBS Lett* (1994) 356: 244-248.
18. Bazan, J.F. (1990) *Proc Natl Acad Sci USA*, 87, 6934-8
- 10 19. de Vos, A.M., Ultsch, M. and Kossiakoff, A.A. (1992) *Science*, 255, 306-12
- 15 20. Layton, M.J., Cross, B.A., Metcalf, D., Ward, L.D., Simpson, R.J. and Nicola, N.A. (1992) *Proceedings of the National Academy of Sciences of the United States of America* 89: 8616-8620
- 20 21. Taga, T., Hibi, M., Hirata, T., Tamasaki, K., Tasukawa, K., Matsuda, T., Hirano, T. and Kishimoto, T. (1989) *Cell* 58: 573-581
- 25 22. Merberg, D.M., Wolf, S.F. and Clark, S.C. (1992) Sequence similarity between NKSF and the IL-6/G-CSF family (1992) *Immunology Today* 13: 77-78
23. Cearing, D.P. and Cosman, D. (1991) *Cell* 66:9-10
- 30 24. Wrighton, N.C., Farrell, F.X., Chang, R., Kashyap, A.K., Barbone, F.P., Mulcahy, L.S., Johnson, D.L., Barrett, R.W., Jolliffe, L.K. and Dower, W.J. (1996) *Science* 273: 458-464.
- 35 25. Cwirla, S.E., Balasubramanian, P., Duffin, D.J., Wagstrom, C.R., Gates, C.M., Singer, S.C., Davis, A.M., Tansik, R.L., Mattheakis, L.C., Boytos, C.M., Schatz, P.J., Baccanari, D.P., Wrighton, N.C., Barret, R.W. and Dower, W.J. (1997) *Science* 276:

1696--9, 1997

26. Samuel Davis et al (1996) *Cell* 87:1161-1169.
- 5 27. Chitra Suri et al (1996) *Cell* 87: 1171-1180.
28. Nicholas C. Wrighton et al (1996) *Science* 273: 458-463.
- 10 29. Oded Livnah et al (1996) *Science* 273: 464-471.
30. Cwirla, Steven E. et al (1997) *Science* 276: 1696-1699.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: (Other than US) AMRAD OPERATIONS PTY LTD

10 (US only) Douglas James HILTON, Nicos Antony NICOLA, Alison FARLEY, Tracey WILLSON, Jian-Guo ZHANG, Warren ALEXANDER, Steven RAKAR, Louis FABRI, Tetsuo KOJIMA, Masatsugu MAEDA, Yasumfumi KIKUCHI, Andrew NASH

15

(ii) TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME

(iii) NUMBER OF SEQUENCES: 39

(iv) CORRESPONDENCE ADDRESS:

20

- (A) ADDRESSEE: DAVIES COLLISON CAVE
- (B) STREET: 1 LITTLE COLLINS STREET
- (C) CITY: MELBOURNE
- (D) STATE: VICTORIA
- (E) COUNTRY: AUSTRALIA

25

- (F) ZIP: 3000

(v) COMPUTER READABLE FORM:

30

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version

#1.25

(vi) CURRENT APPLICATION DATA:

35

(A) APPLICATION NUMBER:

PCT INTERNATIONAL APPLICATION

(B) FILING DATE: 11-SEP-1997

5 (vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PO2246/96

(B) FILING DATE: 11-SEP-1996

10 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HUGHES DR, E JOHN L

(C) REFERENCE/DOCKET NUMBER: EJH/AF

15 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: +61 3 9254 2777

(B) TELEFAX: +61 3 9254 2770

20 15 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

25

Trp Ser Xaa Trp Ser

30 30 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5

ACTCGCTCCA GATTCCCGCC TTTT

24

10 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

25 TCCCGCCTTT TTCGACCCAT AGAT

24

(2) INFORMATION FOR SEQ ID NO:4:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGTACTTGGC TTGGAAGAGG AAAT

24

(2) INFORMATION FOR SEQ ID NO:5:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGCTCACGT GCACGTCGGG TGGG

24

(2) INFORMATION FOR SEQ ID NO:6:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCTGCTGTT AAAGGGCTTC TC

22

35

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- 5 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Oligonucleotide

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

(A/G) CTCCA (A/G) TC (A/G) CTCCA

15

15

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

30

(A/G) CTCCA (C/T) TC (A/G) CTCCA

15

(2) INFORMATION FOR SEQ ID NO:9:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

10

AAGTGTGACC ATCATGTGGA C

21

15 (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

30 GGAGGTGTTA AGGAGGC G

18

(2) INFORMATION FOR SEQ ID NO:11:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

10

ATGCCCGCGG GTCGCCCG

18

15 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1242

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

35	GGCACGAGCT TCGCTGTCCG CGCCCAGTGA CGCGCGTGCG GACCCGAGCC CCAATCTGCA	- 64
	CCCCGCAGAC TCGCCCCCGC CCCATACCGG CGTTGCAGTC ACCGCCCGTT GCGCGCCACC	- 4
	CCC	- 3
	ATG CCC GCG GGT CGC CCG GGC CCC GTC GCC CAA TCC GCG CGG CGG CCG	48

	Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro		
1	5	10	15
	CCG CGG CCG CTG TCC TCG CTG TGG CCT CCT TTG CTC TGT GTC CTC		96
5	Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu		
	20	25	30
	Gly Val Pro Arg Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro		
10	35	40	45
	CAG GAC CCC ACC CTT CTC ATC GGC TCC TCC CTG CAA GCT ACC TGC TCT		144
	Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser		
	50	55	60
15			
	ATA CAT GGA GAC ACA CCT GGG GCC ACC GCT GAG GGG CTC TAC TGG ACC		240
	Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr		
	65	70	75
	60	65	70
20	CTC AAT GGT CGC CGC CTG CCC TCT GAG CTG TCC CGC CTC CTT AAC ACC		288
	Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr		
	85	90	95
	80	85	90
25	TCC ACC CTG GCC CTG GCC CTG GCT AAC CTT AAT GGG TCC AGG CAG CAG		336
	Ser Thr Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln		
	100	105	110
	95	100	105
	90	95	100
30	TCA GGA GAC AAT CTG GTG TGT CAC GCC CGA GAC GGC AGC ATT CTG GCT		384
	Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala		
	115	120	125
	110	115	120
	105	110	115
	100	105	110
	95	100	105
	90	95	100
	85	90	95
	80	85	90
	75	80	85
	70	75	80
	65	70	75
	60	65	70
	55	60	65
	50	55	60
	45	50	55
	40	45	50
	35	40	45
	30	35	40
	25	30	35
	20	25	30
	15	20	25
	10	15	20
	5	10	15
	1	5	10

	AGC TGC TGG TCC CGG AAC ATG AAG GAT CTC ACG TGC CGC TGG ACA CCG	480
	Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro	
145	150	155
		160
5	GGT GCA CAC GGG GAG ACA TTC TTA CAT ACC AAC TAC TCC CTC AAG TAC	528
	Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr	
	165	170
		175
10	AAG CTG AGG TGG TAC GGT CAG GAT AAC ACA TGT GAG GAG TAC CAC ACT	576
	Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr	
	180	185
		190
15	GTG GGC CCT CAC TCA TGC CAT ATC CCC AAG GAC CTG GCC CTC TTC ACT	624
	Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr	
	195	200
		205
20	CCC TAT GAG ATC TGG GTG GAA GCC ACC AAT CGC CTA GGC TCA GCA AGA	672
	Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg	
	210	215
		220
25	TCT GAT GTC CTC ACA CTG GAT GTC CTG GAC GTG GTG ACC ACG GAC CCC	720
	Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro	
	225	230
		235
		240
30	CCA CCC GAC GTG CAC GTG AGC CGC GTT GGG GGC CTG GAG GAC CAG CTG	768
	Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu	
	245	250
		255
35	AGT GTG CGC TGG GTC TCA CCA CCA GCT CTC AAG GAT TTC CTC TTC CAA	816
	Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln	
	260	265
		270
	GCC AAG TAC CAG ATC CGC TAC CGC GTG GAG GAC AGC GTG GAC TGG AAG	864
	Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys	
	275	280
		285

	GTG GTG GAT GAC GTC AGC AAC CAG ACC TCC TGC CGT CTC GCG GGC CTG	912
	Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu	
	290 295 300	
5	AAG CCC GGC ACC GTT TAC TTC GTC CAA GTG CGT TGT AAC CCA TTC GGG	960
	Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly	
	305 310 315 320	
10	ATC TAT GGG TCG AAA AAG GCG GGA ATC TGG AGC GAG TGG AGC CAC CCC	1008
	Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro	
	325 330 335	
15	ACC GCT GCC TCC ACC CCT CGA AGT GAG CGC CCG GGC CCG GGC GGG	1056
	Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly	
	340 345 350	
20	GTG TGC GAG CCG CGG GGC GGC GAG CCC AGC TCG GGC CCG GTG CGG CGC	1104
	Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg	
	355 360 365	
	GAG CTC AAG CAG TTC CTC GGC TGG CTC AAG AAG CAC GCA TAC TGC TCG	1152
	Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser	
	370 375 380	
25	AAC CTT AGT TTC CGC CTG TAC GAC CAG TGG CGT GCT TGG ATG CAG AAG	1200
	Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys	
	385 390 395 400	
30	TCA CAC AAG ACC CGA AAC CAG GTC CTG CCG GCT AAA CTC TAAGGATAGG	1249
	Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu	
	405 410	
	CCATCCTCCT GCTGGTCAG ACCTGGAGGC TCACCTGAAT TGGAGCCCCT CTGTACCATC	1309
35	TGGGCAACAA AGAACCTAC CAGAGGCTGG GGCACAATGA GCTCCCACAA CCACAGCTT	1369
	GGTCCACATG ATGGTCACAC TTGGATATAAC CCCAGTGTGG GTAAGGTTGG GGTATTGCAG	1429

GGCCTCCCAA CAATCTTTT AAATAAATAA AGGAGTTGTT CAGGTAAAAA AAAAAAAAAA 1489

AAAAAAAAAA AAAAAAAA

1506

5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 413 amino acids

10 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro
1 5 10 15

20 Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
20 25 30

Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
35 40 45

25 Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
50 55 60

30 Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
65 70 75 80

Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
85 90 95

35 Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln
100 105 110

Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala
115 120 125

Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile
5 130 135 140

Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro
145 150 155 160

10 Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr
165 170 175

Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr
180 185 190

15 Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr
195 200 205

Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg
20 210 215 220

Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
225 230 235 240

25 Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
245 250 255

Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
260 265 270

30 Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
275 280 285

Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
35 290 295 300

Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
305 310 315 320

Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
5 325 330 335

Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
340 345 350

10 Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
355 360 365

Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
370 375 380

15 Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
385 390 395 400

Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu
20 405 410

(2) INFORMATION FOR SEQ ID NO:14:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

5 GGCACGAGCT TCGCTGTCCG CGCCCAGTGA CGCGCGTGCG GACCCGAGCC CCAATCTGCA -65
 CCCCGCAGAC TCGCCCCCGC CCCATACCGG CGTTGCAGTC ACCGCCCGTT GCGCGCCACC -5
 CCCA -1
 10 ATG CCC GCG GGT CGC CCG GGC CCC GTC GCC CAA TCC GCG CGG CGG CCG 48
 Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro
 1 5 10 15
 15 CCG CGG CCG CTG TCC TCG CTG TGG TCG CCT CTG TTG CTC TGT GTC CTC 96
 Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
 20 25 30
 20 GGG GTG CCT CGG GGC GGA TCG GGA GCC CAC ACA GCT GTA ATC AGC CCC 144
 Gly Val Pro Arg Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
 35 40 45
 25 CAG GAC CCC ACC CTT CTC ATC GGC TCC TCC CTG CAA GCT ACC TGC TCT 192
 Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
 50 55 60
 30 ATA CAT GGA GAC ACA CCT GGG GCC ACC GCT GAG GGG CTC TAC TGG ACC 240
 Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
 65 70 75 80
 35 CTC AAT GGT CGC CGC CTG CCC TCT GAG CTG TCC CGC CTC CTT AAC ACC 288
 Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
 85 90 95
 35 TCC ACC CTG GCC CTG GCC CTG GCT AAC CTT AAT GGG TCC AGG CAG CAG 336
 Ser Thr Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln
 100 105 110

	AGT GTG CGC TGG GTC TCA CCA CCA GCT CTC AAG GAT TTC CTC TTC CAA	816		
	Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln			
	260	265	270	
5	GCC AAG TAC CAG ATC CGC TAC CGC GTG GAG GAC AGC GTG GAC TGG AAG	864		
	Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys			
	275	280	285	
10	GTG GTG GAT GAC GTC AGC AAC CAG ACC TCC TGC CGT CTC GCG GGC CTG	912		
	Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu			
	290	295	300	
15	AAG CCC GGC ACC GTT TAC TTC GTC CAA GTG CGT TGT AAC CCA TTC GGG	960		
	Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly			
	305	310	315	320
20	ATC TAT GGG TCG AAA AAG GCG GGA ATC TGG AGC GAG TGG AGC CAC CCC	1008		
	Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro			
	325	330	335	
	ACC GCT GCC TCC ACC CCT CGA AGT GAG CGC CCG GGC CCG GGC GGG	1056		
	Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly			
	340	345	350	
25	GTG TGC GAG CCG CGG GGC GAG CCC AGC TCG GGC CCG GTG CGG CGC	1104		
	Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg			
	355	360	365	
30	GAG CTC AAG CAG TTC CTC GGC TGG CTC AAG AAG CAC GCA TAC TGC TCG	1152		
	Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser			
	370	375	380	
35	AAC CTT AGT TTC CGC CTG TAC GAC CAG TGG CGT GCT TGG ATG CAG AAG	1200		
	Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys			
	385	390	395	400

	TCA CAC AAG ACC CGA AAC CAG GAC GAG GGG ATC CTG CCT TCG GGC AGA	1248	
	Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly Arg		
	405	410	415
5	CGG GGT GCG GCG AGA GGT CCT GCC GGT TAAACTCTAA GGATAGGCCA	1295	
	Arg Gly Ala Ala Arg Gly Pro Ala Gly		
	420	425	
10	TCCTCCTGCT GGGTCAGACC TGGAGGCTCA CCTGAATTGG AGCCCTCTG TACCATCTGG	1355	
	GCAACAAAGA AACCTACCAAG AGGCTGGGGC ACAATGAGCT CCCACAACCA CAGCTTTGGT	1415	
	CCACATGATG GTCACACTTG GATATACCCC AGTGTGGGTA AGGTTGGGGT ATTGCAGGGC	1475	
15	CTCCCAACAA TCTCTTAAA TAAATAAAGG AGTTGTTAG GTAAAAAAAAA AAAAAAAAAA	1535	
	AAAAAAAAAA.AAAA	1549	

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

	Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro			
	1	5	10	15
35	Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu			
	20	25	30	

Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
35 40 45

Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
5 50 55 60

Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
65 70 75 80

10 Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
85 90 95

Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln
100 105 110

15 Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala
115 120 125

Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile
20 130 135 140

Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro
145 150 155 160

25 Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr
165 170 175

Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr
180 185 190

30 Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr
195 200 205

Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg
35 210 215 220

Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
225 230 235 240

Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
5 245 250 255

Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
260 265 270

10 Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
275 280 285

Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
290 295 300

15 Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
305 310 315 320

Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
20 325 330 335

Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
340 345 350

25 Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
355 360 365

Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
370 375 380

30 Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
385 390 395 400

Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly Arg
35 405 410 415

Arg Gly Ala Ala Arg Gly Pro Ala Gly

420

425

5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 938 base pairs
- 10 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..468

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

25	GGC ACC GTT TAC TTC GTC CAA GTG CGT TGT AAC CCA TTC GGG ATC TAT	48
	Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr	
	1 5 10 15	
	GGG TCG AAA AAG GCG GGA ATC TGG AGC GAG TGG AGC CAC CCC ACC GCT	96
30	Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala	
20	25 30	
	GCC TCC ACC CCT CGA AGT GAG CGC CCG GGC CCG GGC GGG GTG TGC	144
	Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Val Cys	
35	35 40 45	

	GAG CCG CGG GGC GGC GAG CCC AGC TCG GGC CCG GTG CGG CGC GAG CTC	192
	Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu	
	50 55 60	
5	AAG CAG TTC CTC CGC TGG CTC AAG AAG CAC GCA TAC TGC TCG AAC CTT	240
	Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu	
	65 70 75 80	
10	AGT TTC CGC CTG TAC GAC CAG TGG CGT GCT TGG ATG CAG AAG TCA CAC	288
	Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His	
	85 90 95	
15	AAG ACC CGA AAC CAG GTA GGA AAG TTG GGG GAG GCT TGC GTG GGG GGT	336
	Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly	
	100 105 110	
20	AAA GGA GCA GAG GAA GAG AGA GAC CCG GGT GAG CAG CCT CCA CAA CAC	384
	Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His	
	115 120 125	
	CGC ACT CTT CTT TCC AAG CAC AGG ACG AGG GGA TCC TGC CCT CGG GCA	432
	Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala	
	130 135 140	
25	GAC GGG GTG CGG CGA GAG GTA AGG GGG TCT GGG TGAGTGGGGC CTACAGCAGT	485
	Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly	
	145 150 155	
30	CTAGATGAGG CCCTTCCCCC TCCTTCGGTG TTGCTCAAAG GGATCTCTTA GTGCTCATTT	545
	CACCCACTGC AAAGAGCCCC AGGTTTTACT GCATCATCAA GTTGCTGAAG GGTCCAGGCT	605
	TAATGTGGCC TCTTTCTGC CCTCAGGTCC TGCCGGCTAA ACTCTAAGGA TAGGCCATCC	665
35	TCCTGCTGGG TCAGACCTGG AGGCTCACCT GAATTGGAGC CCCTCTGTAC CTATCTGGGC	725
	AACAAAGAAA CCTACCATGA GGCTGGGGCA CAATGAGCTC CCACAACCAC AGCTTTGGTC	785

CACATGATGG TCACACTTGG ATATACCCCA GTGTGGGTAA GGTTGGGGTA TTGCAGGGCC 845
 TCCCAACAAT CTCTTTAAAT AAATAAAGGA GTTGTTCAGG TAAAAAAAAA AAAAAAAA 905
 AAAAAAAA AAAAAAAA AAAAAAAA AAA 938

(2) INFORMATION FOR SEQ ID NO:17:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

	Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe	Gly	Ile	Tyr
20	1				5					10					15	

Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala
20 25 30

25 Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Val Cys
 35 40 45

Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu
50 55 60

30 Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu
65 70 75 80

Ser	Phe	Arg	Leu	Tyr	Asp	Gln	Trp	Arg	Ala	Trp	Met	Gln	Lys	Ser	His
35							85				90				95

Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly
100 105 110

Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His
5 115 120 125

Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala
130 135 140

10 Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly
145 150 155

15 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..834

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCC ACC CTT CTC ATC GGC TCC TCC CTG CAA GCT ACC TGC TCT ATA CAT
Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His
35 51 55 60 65

98

	GGA GAC ACA CCT GGG GCC ACC GCT GAG GGG CTC TAC TGG ACC CTC AAT	146	
	Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn		
	70	75	80
5	GGT CGC CGC CTG CCC TCT GAG CTG TCC CGC CTC CTT AAC ACC TCC ACC	194	
	Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr		
	85	90	95
10	CTG GCC CTG GCC CTG GCT AAC CTT AAT GGG TCC AGG CAG CAG TCA GGA	242	
	Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser Gly		
	100	105	110
15	GAC AAT CTG GTG TGT CAC GCC CGA GAC GGC AGC ATT CTG GCT GGC TCC	290	
	Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser		
	115	120	125
	130		
20	TGC CTC TAT GTT GGC TTG CCC CCT GAG AAG CCC TTT AAC ATC AGC TGC	338	
	Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser Cys		
	135	140	145
	150		
	TGG TCC CGG AAC ATG AAG GAT CTC ACG TGC CGC TGG ACA CCG GGT GCA	386	
	Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala		
	155	200	
25	CAC GGG GAG ACA TTC TTA CAT ACC AAC TAC TCC CTC AAG TAC AAG CTG	434	
	His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu		
	205	210	215
30	AGG TGG TAC GGT CAG GAT AAC ACA TGT GAG GAG TAC CAC ACT GTG GGG	482	
	Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly		
	220	225	230
35	CCC CAC TCA TGC CAT ATC CCC AAG GAC CTG GCC CTC TTC ACT CCC TAT	530	
	Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr		
	235	240	245
	250		

	GAG ATC TGG GTG GAA GCC ACC AAT CGC CTA GGC TCA GCA AGA TCT GAT	578		
	Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp			
	255	260	265	
5	GTC CTC ACA CTG GAT GTC CTG GAC GTG GTG ACC ACG GAC CCC CCA CCC	626		
	Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro Pro Pro			
	270	275	280	
10	GAC GTG CAC GTG AGC CGC GTT GGG GGC CTG GAG GAC CAG CTG AGT GTG	674		
	Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val			
	285	290	295	
15	CGC TGG GTC TCA CCA CCA GCT CTC AAG GAT TTC CTC TTC CAA GCC AAG	722		
	Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys			
	300	305	310	
20	TAC CAG ATC CGC TAC CGC GTG GAG GAC AGC GTG GAC TGG AAG GTG GTG	770		
	Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val			
	315	320	325	330
	GAT GAC GTC AGC AAC CAG ACC TCC TGC CGT CTC GCG GGC CTG AAG CCC	818		
	Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro			
	335	340	345	
25	GGC ACC GTT TAC TTC GTC CAA GTG CGT TGT AAC CCA TTC GGG ATC TAT	866		
	Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr			
	350	355	360	
30	GGG TCG AAA AAG GCG GGA	894		
	Gly Ser Lys Lys Ala Gly			
	365			

(2) INFORMATION FOR SEQ ID NO:19:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His
10 51 55 60 65

Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn
70 75 80

15 Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr
85 90 95

Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser Gly
100 105 110

20 Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser
115 120 125 130

Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser Cys
25 135 140 145

Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala
150 155 200

30 His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu
205 210 215

Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly
220 225 230

35 Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr
235 240 245 250

Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp
255 260 265

Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro Pro Pro
5 270 275 280

Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val
285 290 295

10 Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys
300 305 310

Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val
315 320 325 330

15 Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro
335 340 345

Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
20 350 355 360

Gly Ser Lys Lys Ala Gly
365

25

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 143 base pairs
30 (B) TYPE: nucleic acids
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCATGAAGG CTTAGGGTGG GGATCGGTAG GACCCATGCA CCCAGAGAAA GGGACTGGTG 60

GCAACTTCA AACTCTCTGG GGAAGGAAGA AGGGCTGAAA GAGG 104

5 ATG AAC GGG CTC AGA CAC AGC TGT AAT CAG CCC CCA GGA 143

Met Asn Gly Leu Arg His Ser Cys Asn Gln Pro Pro Gly

5 10

10 (2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acids

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

20

Met Asn Gly Leu Arg His Ser Cys Asn Gln Pro Pro Gly

5 10

25

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1930 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

	GGCACGAGCT TCGCTGTCCG CGCCCAGTGA CGCGCGTGCG GACCCGAGCC CCAATCTGCA	60
5	CCCCGCAGAC TCGCCCCCGC CCCATACCGG CGTTGCAGTC ACCGCCCGTT GCGGCCACC	120
	CCCAATGCC C GCGGGTCGCC CGGGCCCCGT CGCCAATCC GCGCGGCCGGC CGCCGCGGCC	180
	GCTGTCTCG CTGTGGTCGC CTCTGTTGCT CTGTGTCTC GGGGTGCCTC GGGGCGGATC	240
10	GGGAGCCCAC ACAGCTGTAA TCAGCCCCA GGACCCCACC CTTCTCATCG GCTCCTCCCT	300
	GCAAGCTACC TGCTCTATAAC ATGGAGACAC ACCTGGGGCC ACCGCTGAGG GGCTCTACTG	360
15	GACCCCTCAAT GGTCGCCGCC TGCCCTCTGA GCTGTCCCAC CTCCTTAACA CCTCCACCCCT	420
	GGCCCTGGCC CTGGCTAACC TTAATGGGTC CAGGCAGCAG TCAGGAGACA ATCTGGTGTG	480
	TCACGCCCGA GACGGCAGCA TTCTGGCTGG CTCCTGCCTC TATGTTGGCT TGCCCCCTGA	540
20	GAAGCCCTTT AACATCAGCT GCTGGTCCCG GAACATGAAG GATCTCACGT GCCGCTGGAC	600
	ACCGGGTGCA CACGGGGAGA CATTCTTACA TACCAACTAC TCCCTCAAGT ACAAGCTGAG	660
25	GTGGTACGGT CAGGATAACA CATGTGAGGA GTACCACACT GTGGGGCCCTC ACTCATGCCA	720
	TATCCCCAAG GACCTGGCCC TCTTCACTCC CTATGAGATC TGGGTGGAAG CCACCAATCG	780
	CCTAGGCTCA GCAAGATCTG ATGTCCTCAC ACTGGATGTC CTGGACGTGG TGACCACGGA	840
30	CCCCCCACCC GACGTGCACG TGAGCCGCGT TGGGGCCCTG GAGGACCAGC TGAGTGTGCG	900
	CTGGGTCTCA CCACCAGCTC TCAAGGATTT CCTCTTCCAA GCCAAGTACC AGATCCGCTA	960
35	CCCGCGTGGAG GACAGCGTGG ACTGGAAGGT GGTGGATGAC GTCAGCAACC AGACCTCCTG	1020
	CCGTCTCGCG GGCCTGAAGC CCGGCACCGT TTACTTCGTC CAAGTGCCTT GTAACCCATT	1080

	CGGGATCTAT GGGTCGAAAA AGGCAGGAAT CTGGAGCGAG TGGAGCCACC CCACCGCTGC	1140
	CTCCACCCCT CGAAGTGAGC GCCCGGGCCC GGGCGGCAGG GTGTGCGAGC CGCGGGCGG	1200
5	CGAGCCCAGC TCGGGCCCCG TGCGGCGCGA GCTCAAGCAG TTCTCGGCT GGCTCAAGAA	1260
	GCACGCATAC TGCTCGAACCC TTAGTTCCG CCTGTACGAC CAGTGGCGTG CTTGGATGCA	1320
	GAAGTCACAC AAGACCCGAA ACCAGGTAGG AAAGTTGGGG GAGGCTTGCG TGGGGGTAA	1380
10	AGGAGCAGAG GAAGAGAGAG ACCCGGGTGA GCAGCCTCCA CAACACCGCA CTCTCTTTC	1440
	CAAGCACAGG ACGAGGGGAT CCTGCCCTCG GGCAGACGGG GTGCGGCGAG AGGTAAGGGG	1500
15	GTCTGGGTGA GTGGGGCCTA CAGCAGTCTA GATGAGGCCCTTCC TTCTGGTGTG	1560
	CTCAAAGGGA TCTCTTAGTG CTCATTTCAC CCACTGCAAA GAGCCCCAGG TTTIACTGCA	1620
	TCATCAAGTT GCTGAAGGGT CCAGGCTTAA TGTGGCCTCT TTTCTGCCCT CAGGTCCCTGC	1680
20	CGGCTAAACT CTAAGGATAG GCCATCCTCC TGCTGGGTCA GACCTGGAGG CTCACCTGAA	1740
	TTGGAGCCCC TCTGTACCTA TCTGGCAAC AAAGAAACCT ACCATGAGGC TGGGGCACAA	1800
25	TGAGCTCCCA CAACCACAGC TTTGGTCCAC ATGATGGTCA CACTTGGATA TACCCAGTG	1860
	TGGGTAAAGGT TGGGGTATTG CAGGGCCTCC CAACAATCTC TTTAAATAAA TAAAGGAGTT	1920
	GTTCAGGTAA	1930
30		

(2) INFORMATION FOR SEQ ID NO:23:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 560 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

10	TCCAGGCAGC GGTCGGGGGA CAACCTCGTG TGCCACGCC GTGACGGCAG CATCCTGGCT	60
	GGCTCCTGCC TCTATGTTGG CCTGCCCCA GAGAAACCCG TCAACATCAG CTGCTGGTCC	120
	AAGAACATGA AGGACTTGAC CTGCCGCTGG ACGCCAGGGG CCCACGGGA GACCTTCCTC	180
15	CACACCAACT ACTCCCTCAA GTACAAGCTT AGGTGGTATG GCCAGGACAA CACATGTGAG	240
	GAGTACCACA CAGTGGGCC CCACTCCTGC CACATCCCCA AGGACCTGGC TCTCTTTACG	300
20	CCCTATGAGA TCTGGGTGGA GGCCACCAAC CGCCTGGCT CTGCCCGCTC CGATGTACTC	360
	ACGCTGGATA TCCTGGATGT GGTGACCACG GACCCCCCGC CCGACGTGCA CGTGAGCCGC	420
	GTCGGGGGCC TGGAGGACCA GCTGAGCGTG CGCTGGGTGT CGCCACCCGC CCTCAAGGAT	480
25	TTCCCTTTTC AAGCCAAATA CCAGATCCGC TACCGAGTGG AGGACAGTGT GGAATGGAAG	540
	GTGGTGGACG ATGTGAGCAA	560
30		

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1391 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 5 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

10	ACC CTC AAC GGG CGC CGC CTG CCC CCT GAG CTC TCC CGT GTA CTC AAC	48
	Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn	
	1 5 10 15	
15	GCC TCC ACC TTG GCT CTG GCC CTG GCC AAC CTC AAT GGG TCC AGG CAG	96
	Ala Ser Thr Leu Ala Leu Ala Leu Asn Leu Asn Gly Ser Arg Gln	
	20 25 30	
20	CGG TCG GGG GAC AAC CTC GTG TGC CAC GCC CGT GAC GGC AGC ATC CTG	144
	Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu	
	35 40 45	
25	GCT GGC TCC TGC CTC TAT GTT GGC CTG CCC CCA GAG AAA CCC GTC AAC	192
	Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn	
	50 55 60	
30	ATC AGC TGC TGG TCC AAG AAC ATG AAG GAC TTG ACC TGC CGC TGG ACG	240
	Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr	
	65 70 75 80	
35	CCA GGG GCC CAC GGG GAG ACC TTC CTC CAC ACC AAC TAC TCC CTC AAG	288
	Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys	
	85 90 95	
	TAC AAG CTT AGG TGG TAT GGC CAG GAC AAC ACA TGT GAG GAG TAC CAC	336
	Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His	
	100 105 110	

	ACA GTG GGG CCC CAC TCC TGC CAC ATC CCC AAG GAC CTG GCT CTC TTT		384
	Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe		
	115	120	125
5	ACG CCC TAT GAG ATC TGG GTG GAG GCC ACC AAC CGC CTG GGC TCT GCC		432
	Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala		
	130	135	140
10	CGC TCC GAT GTA CTC ACG CTG GAT ATC CTG GAT GTG GTG ACC ACG GAC		480
	Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp		
	145	150	155
			160
15	CCC CCG CCC GAC GTG CAC GTG AGC CGC GTC GGG GGC CTG GAG GAC CAG		528
	Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln		
	165	170	175
20	CTG AGC GTG CGC TGG GTG TCG CCA CCC GCC CTC AAG GAT TTC CTC TTT		576
	Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe		
	180	185	190
25	CAA GCC AAA TAC CAG ATC CGC TAC CGA GTG GAG GAC AGT GTG GAC TGG		624
	Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp		
	195	200	205
30	AAG GTG GTG GAC GAT GTG AGC AAC CAG ACC TCC TGC CGC CTG GCC GGC		672
	Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly		
	210	215	220
35	CTG AAA CCC GGC ACC GTG TAC TTC GTG CAA GTG CGC TGC AAC CCC TTT		720
	Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe		
	225	230	235
			240
	GGC ATC TAT GGC TCC AAG AAA GCC GGG ATC TGG AGT GAG TGG AGC CAC		768
	Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His		
	245	250	255

CCC ACA GCC GCC TCC ACT CCC CGC AGT GAG CGC CCG GGC CCG GGC GGC		816
Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly		
260	265	270
5 GGG GCG TGC GAA CCG CGG GGC GGA GAG CCG AGC TCG GGG CCG GTG CGG		864
Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg		
275	280	285
CGC GAG CTC AAG CAG TTC CTG GGC TGG CTC AAG AAG CAC GCG TAC TGC		912
Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys		
290	295	300
TCC AAC CTC AGC TTC CGC CTC TAC GAC CAG TGG CGA GCC TGG ATG CAG		960
Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln		
5 305	310	315
320		
AAG TCG CAC AAG ACC CGC AAC CAG CAC AGG ACG AGG GGA TCC TGC CCT		1008
Lys Ser His Lys Thr Arg Asn Gln His Arg Thr Arg Gly Ser Cys Pro		
325	330	335
CGG GCA GAC GGG GCA CGG CGA GAG GTC CTG CCA GAT AAG CTG TAGGGCTCA		1060
Arg Ala Asp Gly Ala Arg Arg Glu Val Leu Pro Asp Lys Leu		
340	345	350
5 GGCCACCCCTC CCTGCCACGT GGAGACGCAG AGGCCGAACC CAAACTGGGG CCACCTCTGT		1120
ACCCCTCACTT CAGGGCACCT GAGCCCCCTCA GCAGGGAGCTG GGGTGGCCCC TGAGCTCCAA		1180
CGGCCATAAC AGCTCTGACT CCCACGTGAG GCCACCTTTG GGTGCACCCCC AGTGGGTGTG		1240
0 TGTGTGTGTG TGAGGGTTGG TTGAGTTGCC TAGAACCCCT GCCAGGGCTG GGGGTGAGAA		1300
GGGGAGTCAT TACTCCCCAT TACCTAGGGC CCCTCCAAAA GAGTCCTTTT AAATAAATGA		1360
5 GCTATTTAGG TGCAAAAAAA AAAAAAAA A		1391

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 350 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn
1 5 10 15

15 Ala Ser Thr Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
20 25 30

Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
35 40 45

20 Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn
50 55 60

25 Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
65 70 75 80

Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
85 90 95

30 Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
100 105 110

Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
115 120 125

35 Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
130 135 140

Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp
145 150 155 160

Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln
5 165 170 175

Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe
180 185 190

10 Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp
195 200 205

Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
210 215 220

15 Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe
225 230 235 240

Gly Ile Tyr Gly Ser Lys Ala Gly Ile Trp Ser Glu Trp Ser His
20 245 250 255

Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
260 265 270

25 Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg
275 280 285

Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys
290 295 300

30 Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
305 310 315 320

Lys Ser His Lys Thr Arg Asn Gln His Arg Thr Arg Gly Ser Cys Pro
35 325 330 335

Arg Ala Asp Gly Ala Arg Arg Glu Val Leu Pro Asp Lys Leu
340 345 350

5 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCCAGGCAGC GGTCGGGGGA CAAC

24

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

35 TTGCTCACAT CGTCCACCA CTTG

24

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 6663 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

15	CCCAGAACTC TTGGACGCTG AGGCAGGAGG ATTCCCAAGT TTCAAGACAG TGTGTTCTA	60
	GGTAATGAGA CCCTGTCAAG AAAAGAAAAG AAATAAAAGAG ACAAGAAAAT GTTTATAGGC	120
	TGTGAGACAG CTTGGTGGGT AAGGGGCACT TGCTCCAAT CAAGATGACC TCAGCCCCAT	180
20	CCCTAGGAAT CCATGGTAGA AGGAGAAAGC AAACTCGCAG CTGCTGACCT CCATACATGT	240
	GCTCCAATGT GCACACACAC AGGGAGACAT AATCAATTAA TAGGATGTAT TTGCTTAGAT	300
25	TTGAGTAGGC ATTTATGACT GATGTTTAA AATTTTTATT TGATTITATG AAAATATACC	360
	TGTTTGTATT TGGTTTGGTT TGGTTTGAGT TTTGTTTATT TGAGACAGGG CTTCTCTGTG	420
	TAGTCCTGGC TGTCCCTGGA ACTCACTCTG TAGACCAGGC TGGCCTTGAA CTCAGAAATC	480
30	CGCCTGCTTG TGCTTCCAA GTGCTTAGAT TAAAGGTGTG CACTGCCATT CAGCAAAATT	540
	GCATACTTTA ACCCCAGTAT TTGGGAGGCA GAGGCAGACT AATGTGTGAA TTCCAGGCTA	600
35	GCCAAGGATA CAGAGTGAGA CCCTATTCTT ACCCTCCCCC CCCAAAACCC CAAAATGTAT	660
	TTTGTGCTTG TGTATGTACA TGTGTGTTGC AGCACGTAAA TGTCCAAGGA CAACTTGTAG	720

	AAGTTCTCTC CGTTCACAGT CTAAGTCCTG AATTCAAAC T AAGGTCTCA GGCTTAGCCA	780
	CAGTCTTCTT TATGTACTGA GCCATTACAC TGGCCCTGGA TTGACTGATG AATTAATTT	840
5	TGAGATAAGG TCTCTTGAT GCTCTAGCTAG GCTCAAAC TA TGAACTCCC AGGTCACTTT	900
	GAGCTGCTGG TACTCTTGCT TCCACCCCAA GTGGTGGAAAT GATACTCAGG CAGCACTTCT	960
	CTGGGGAAAGG GGCTGGCCTT GGCTTGATT TTGTTGCCTC AGCTTCAATG AGTGCTTGGG	1020
10	TCTCGTTGTT TCTTTCTTT ATCTGTGAAA TGGGTGAACA CCTGTTCAAG ACTTCCTGAC	1080
	TCTTGAAACA TCCAGGCAGG GTGAGGGACT TGAAGTGGC TCATCCCAG CCTAACAAAG	1140
15	TGTCGTCTT GACCCCAGAC ACAGCTGTAA TCAGCCCCA GGACCCACC CTTCTCATCG	1200
	GCTCCTCCCT GCAAGCTACC TGCTCTATAC ATGGAGACAC ACCTGGGCC ACCGCTGAGG	1260
	GGCTCTACTG GACCTTCAAT GGTCGCCGCC TGCCCTCTGA GCTGTCCCGC CTCCTTAACA	1320
20	CCTCCACCCCT GGCCCTGGCC CTGGCTAAC C TTAATGGGT CAGGCAGCAG TCAGGAGACA	1380
	ATCTGGTGTG TCACGCCGA GACGGCAGCA TTCTGGCTGG CTCCTGCCTC TATGTTGGCT	1440
25	GTAAGTGGGG CCCCAGACAC TCAGAGATAG ATGGGGGTG GCAATGACAG ATTTAGAGCC	1500
	TGGGTCTTCT GTCCTGGGGC AGAGCCATGG GCTCTCACTT GCATGCAGGC ATGGTCATAC	1560
	CCAGCACAGG CATTGCAACT CTAGGGACAG CTGTGGCTGC ACTGTCCCT GTGTACCCCA	1620
30	CAGCTTTAGA AAAGCTGTCA TGTTTCCTT GTAGTGCCCC CTGAGAAGCC CTTAACATC	1680
	AGCTGCTGGT CCCGGAACAT GAAGGATCTC ACGTGCCGCT GGACACCGGG TGCACACGGG	1740
35	GAGACATTCT TACATACCAA CTACTCCCTC AAGTACAAGC TGAGGTTGGT ACCCAGCCAA	1800
	GCCTTGCTGT GTGACTTCTG GCAATACTTA CCTTCTCTGA TCAAATATGT TCCTGTTAT	1860

	GAACTCAAAA GGGACTCTCG CACCTCCACA GGTGGTACGG TCAGGATAAC ACATGTGAGG	1920
	AGTACCACAC TGTGGGCCCT CACTCATGCC ATATCCCCAA GGACCTGGCC CTCTTCACTC	1980
5	CCTATGAGAT CTGGGTGGAA GCCACCAATC GCCTAGGCTC AGCAAGATCT GATGTCCCTCA	2040
	CACTGGATGT CCTGGACGTG GGTGAGCCCC CAGTGTCCAC CTGTGTTCTG CCCTAGACCT	2100
	TATAGGGCGC CTCCCCCCA TCCCCCAGA CTTTTGGTT CTTCTAGAGG TCTTAGCCAC	2160
10	AGCCACGGTG GTTGCAGGAC AGTGGTTGTT CATAACTTAA TGCAAAGACT TTCCCCCCAAG	2220
	ACAGTCAAGA TTTTCCCCT CCCCCCCCCC AACACACACA TACACACACA CTCTGCAGAG	2280
15	AACACCTGGC CTGACCACCC TCCCTCTCTA CAGCCCAGGT GTTCAGAAGG GAGTCCTAGG	2340
	GGACTGAGAG GAGGCAGCCA GGTCTGAAGG CGCCCCAGGA AGCCGAGGCC TTGAGCTGG	2400
	GGGGGGGGCG AGGGTTGGAG GCACGAAC TGATGATCCCT GAGCACAACT GGGCCTAAC	2460
20	TAATTAGGGT GTTCCCAGCC CAAAGCAGCC TGGGCCATT AACCTTCAA GTGCCTCACT	2520
	GAAGACTCAG GGGAGAGATC AGCTTGTACT CTCTCCATGG TCCCCCAGGA GGGTTCTGG	2580
25	GTGCCCTGG CTCATTCCCA CATCCAGAGG TTTTGTGTCT TCCTGGCATC TAACCCTCAG	2640
	TTGTGCTCTG TGGCTGGCAC AGCTGCCCG TGGAGGCTCT TGTAATGTA CAAGGCATCA	2700
	GAGGTGGACA TGGGATGGGG ATACATAGGG ATGGAGCCAA ATAGCACCTC AAGGTGGGGT	2760
30	GATATACAAT AAAGCTTGTC ACCCTGACGC TCAGAAAGCC TACTCATGAT GATCACAAATT	2820
	GTGACATCA CTCTGGACA TGTAGTGAGA CCCTAGCTCA AAACACAGAC AGTAGCTTTA	2880
35	AGAGTCAGCT TGTGACTTAA TACTGGAAC CAGGGCCTAA TAGGTGCTGG GTGATGCTCG	2940
	CCTCACTCCC TGTTTAGTGA GATCTCTGCG CTAATCTCCA CCCCAGCTGG GTGGGCTGCT	3000

	CTGTCCCCCTT GAGGGCAGGA ATGTGTGTCT TCCATCAGAG ATAGGACCCG TGGTAGCAGC	3060
	AACTGCTGCT GGCTGTTCT GGAATATTAA ATGACAGTAA TCTATCAGGC CTGGGTGAGT	3120
5	AGCTAACAGG GGTGGGGCG TGGCTGGAA AACGCAGATA GGGTCATAGG AGCCACTGCA	3180
	GCCTAGATTA CACCACTGGG TGTTCTGTCA CTAGGCCATT CTCACCAAGC AGTCCTCAGA	3240
	ACTGGGAGCA CTGTTGCCAG CATTAAATGC CAGCATTAA TGCCAGCATT AGGGGAGGCA	3300
10	GAGGCAGAAG GATCTCTCTG AGTTCAAGGC CATCCTGAAT TTACATAAAG AGCTCCAGGC	3360
	CAGCCAGGGT GCGCAGTAAA ACCTTGTCTC AAAAAACAAA GCATCTTAG TGACCAGGCT	3420
15	TGCTCCACCC CCAGTGACCA CGGACCCCCC ACCCGACGTG CACGTGAGCC GCGTTGGGGG	3480
	CCTGGAGGAC CAGCTGAGTG TGCGCTGGGT CTCACCACCA GCTCTCAAGG ATTTCTCTT	3540
	CCAAGCCAAG TACCAAGATCC GCTACCGCGT GGAGGACAGC GTGGACTGGA AGGTGCCCGT	3600
20	CCCGCCCCGG ACCCGCCCT GACCCCGCCC CCCGCATCTG ACTCCTCCCT CACCGTGCAG	3660
	GTGGTGGATG ACGTCAGCAA CCAGACCTCC TGCCGTCTCG CGGGCCTGAA GCCCGGCACC	3720
25	GTAACTTCG TCCAAGTGCG TTGTAACCCA TTCGGGATCT ATGGGTGAA AAAGGGGGGA	3780
	ATCTGGAGCG AGTGGAGCCA CCCCACCGCT GCCTCCACCC CTCGAAGTGG TGAGCACCTC	3840
	TCCAGGGCTG GCTGGCCCAT GGAATCCCCA ATCCATCCTG TTCCCTCCCC CCCACCCCTT	3900
30	TTTGAGACA GCGTCTTCAG GTAGCGCATG CTGGCCTTAA ATTCAAGTATG TAGTCAAGGA	3960
	TGACCTCGAG CTCCCTGGTCT TTTGTCTCC ACTTAGAGAC AATGGCCAGT GGCCATCACC	4020
35	ACCTTTGGGA GACTAGCCAT GGAGTCTATT TAGCCTGTCA TTTGGTGACA GATGGAGTAC	4080
	AACAGTGTGA CCTCTTGTAA GAGAACTGAA GACAGGCTGT TTTAACCCC AATATCCTAG	4140

	GCTCTCTAGA GGTTAAC TTT ATATAAAATA GAGACTATT AAGCCAGTTA TCACATGGTC	4200
	CCACAGAAC C TTTGTCACA CAACCTATAG ACCACAGTGC CTGTGCCTAC CACATAAGGG	4260
5	TCTCTACTGC TGGCCCACCC CTCCAACCT TAAAAGGTAA CCTAGGCAGC CTTAATATT	4320
	GCAATCCTCC TACCTCAGCC TCTTGAATGC TCAGAAACCA GGCATTAACC CAAGTTCTC	4380
	TTCTCTGGGT CCCTTCTTA AGGTGGGAGG GCCTAAAGAT GACTTCCTT GTCCTGAAGA	4440
10	CTCTCCGAGC CCATGGATCT GCACTCTCTA ATATGAAATA TATTGCATAA AATGTCTGGC	4500
	CTCAGTTCC CCACCTGTCA GGTTAGGCA GCACAGTCGG TCCAAGACAC TTCATTATT	4560
15	GCAGGCAGTA TAAGAAGAAG CTCCCATCCC CCACCCGCTT CCTCCGGTCC CTAAGACAGA	4620
	ATACTTCTAC ACTGAAACTG AACTCTCGCA GACGCATATG CTCACTTAA TGATGATGAA	4680
	ATAATGGGGA AACTGAGGCT CCGAGAGATT CCTGGAGGAA GAGGGTCAA ACCAGCTCCA	4740
20	GGAAGCTCTC CAGCCCCAT CGGGCCCTCT CCAGGTTCTG GGCTTGGCGG GAGTGAACAC	4800
	AGCTGGGAGG GGCTGGAGCC TGGGAGCTTT GGCCCTTGCT CGTGCCAGC ACCTGCGATT	4860
25	CTTGCACGGG AGCCAGCAGG CGGCTCGTC CGCCCGAGAG ACTGAAGAAG CCGGGGGTAG	4920
	GGTTGGAGGG AGGTAAAGCAG GGGCTGTGGG GGCGAAGCT TGTGCCAGGG CCTGTCAGCG	4980
	AGTCCCCAGT TTTATTTATG GCGTGAGGCC GATGTCCTTA TCCGCTGGCC TGCTGGGGA	5040
30	TGGCTGCCGC TGGGGATTGG ACCCAAGGGC TGGCTTCCCA CTCAGTCCTC CAGCCCAC	5100
	CATGTCACAC CCGTGCATTC TCTGAGGCTT ATCTTGGGAA CCCGCCCTG TTCTGTGCTG	5160
35	TCTGTCTCTA TTTCTGTCAT TCACTTCCC AGAGCCTTT TTTTATGCTT TTAATATAAC	5220
	TACGTTTAA AAATTGCTTT TGTATAATGT GTGTGCCTTC GTGAGCGTGC GTGCCACAAC	5280

	ACACACGTGA AGGTTAGAGA ACTTTGTTGA GTAGGCTCCT TCCACCATGT GGGACTAGGG	5340
	CTGGCGACAA GAGCAATTAC TGAGTCATCT CGCCAGCCCC TCACCCCTCA CTTCCCATCC	5400
5	TGTTTGGATA GTCATAGGTA ATCGAAGGTA AATCGCTGGC TTIAATTTCG TAGCTATCCT	5460
	GCCTCAGCCT ACCAAGTGCT GTGCTACAC GTTTGTGGGA GGGGCTCTCC TCCCAGTGTC	5520
	TGGGGGTGAC ACAGTCCCAA GATCTCTGCT TTCTAGGTCT TTGTCTTAGT TTGCCCTTIG	5580
10	CTTTGTCCGT GTCCCTAGAG TCTCCGGCCC CACTTATCCA TTGACTGGTC TTTCCTTTAC	5640
	CGAATACTCG GTTTTACCTC CCACTGATTG GACTCCCTCC TTTGCTTGTGTC TCCATGCCG	5700
15	TGGCATTGCC ATTCCCTCTGG GTGACTCTGG GTCCACACCT GACACCTTTC CCAACTTTCC	5760
	CCAGCCGAAG CTGGTCTGGT ATGGGAGGCC GCCGTCCCGC GCGCGCCTCC TGCTGGCCGC	5820
	GCCCCAACAC TGCCGCTCCA TTCTCTTAG AGCGCCCCGGG CCCGGGCGGC GGGGTGTGCG	5880
20	AGCCCGGGGG CGGCGAGCCC AGCTCGGGCC CGGTGCGGCG CGAGCTCAAG CAGTTCTCG	5940
	GCTGGCTCAA GAAGCACGCA TACTGCTCGA ACCTTAGTTT CCGCCTGTAC GACCAGTGGC	6000
25	GTGCTTGGAT GCAGAAAGTCA CACAAGACCC GAAACCAGGT AGGAAAGTTG GGGGAGGCTT	6060
	GCGTGGGGGG TAAAGGAGCA GAGGAAGAGA GAGACCCGGG TGAGCAGCCT CCACAAACACC	6120
	GCACCTTTCT TTCCAAGCAC AGGACGAGGG GATCCTGCC TCAGGGCAGAC GGGGTGCGGC	6180
30	GAGAGGTAAG GGGGTCTGGG TGAGTGGGC CTACAGCACT CTAGATGAGG CCCTTCCCC	6240
	TCCTTCGGTG TTGCTCAAAG GGATCTCTTA GTGCTCATTT CACCCACTGC AAAGAGCCCC	6300
35	AGGTTTTACT GCATCATCAA GTTGTGAAG GGTCCAGGCT TAATGTGGCC TCTTTCTGC	6360
	CCTCAGGTCC TGCCGGCTAA ACTCTAAGGA TAGGCCATCC TCCTGCTGGG TCAGACCTGG	6420

AGGCTCACCT GAATTGGAGC CCCTCTGTAC CATCTGGCA ACAAAGAAAC CTACCAGAGG 6480
CTGGGCACAA TGAGCTCCCA CAACCACAGC TTTGGTCCAC ATGATGGTCA CACTTGGATA 6540
5 TACCCCAGTG TGGTAGGGT TGGGTATTG CAGGGCCTCC CAAGAGTCTC TTTAAATAAA 6600
TAAAGGAGTT GTTCAGGTCC CGATGCCAG TGTGTTGGG GCCTATGTGC TGGGTGGGG 6660
GGA 6663
10

(2) INFORMATION FOR SEQ ID NO:29:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

25 Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile
1 5 10 15

His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Phe
20 25 30

30

Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser
35 40 45

35 Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser
50 55 60

Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly
65 70 75 80

Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser
5 85 90 95

Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly
100 105 110

10 Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys
115 120 125

Leu Arg Leu Val Arg Ser Gly * His Met * Gly Val Pro His Cys
130 135 140

15 Gly Pro Ser Leu Met Pro Tyr Pro Gln Gly Pro Gly Pro Leu His Ser
145 150 155 160

Leu * Asp Leu Gly Gly Ser His Gln Ser Pro Arg Leu Ser Lys Ile
20 165 170 175

* Cys Pro His Thr Gly Cys Pro Gly Arg
180 185

25

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGCTGGCGCG CCTCCCGGGC GGATCGGGAG CCCAC

35

5 (2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

20 AGCTACGCGT TTAGAGTTA GCCGGCAG

28

(2) INFORMATION FOR SEQ ID NO:32:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

35

Met Val Leu Ala Ser Ser Thr Thr Ser Ile His Thr Met Leu Leu Leu

1

5

10

15

Leu Leu Met Leu Phe His Leu Gly Leu Gln Ala Ser Ile Ser

20

25

30

5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

20

Ile Lys Pro Ser Gly Arg Arg Gly Ala Ala Arg Gly Pro Ala Gly Asp Tyr Lys Asp Asp

5

10

15

20

Asp Asp Lys

25

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

5 GATCTTGCCC TCGGGCAGAC GGGGTGCGGC GAGAGGTCCCT GCCGGCGACT ACAAGGACGA 60
CGATGACAAG TAG 73

10 (2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

25

AACGGGAGCC CGTCTGCCCT ACGCCGCTCT CCAGGACGGC CGCTGATGTT CCTGCTGCTA 60

CTGTTCATCC TAG

73

30

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCCACGCTTC TCATCGGATT CTCCCTG

27

10

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

25

CAGTCCACAC TGTCTCCAC TCGGTAG

27

30

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11832 base pairs
- (B) TYPE: nucleic acid
- 35 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- 119 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

	GCGGCCGCTG CAGTGATTAC TCACCGCGTG GCGCACCCCA CCCGCGGGCC GCTGAGTGGA	60
5	TTTTTCCGTG GGGGGATGTG AAGAAGTTA GGGAGAACTC TTCTGCACCG ATGGGAACTA	120
	GGAATGCAGG GTTCGGTCCC GTTCCCCAAA GGACACACCT CTCCCCATAA GCCCACTCAT	180
10	AAGGGCTCCC TGCACCGCCT CGGGGACATC CCCATATCCA ATACCCGAG ATATGATACT	240
	TGAGAAGGGA CCAGAGGCCG GAGACTCCCT CCCTGCCTTC TGGCTTTCCC CCCCCCTGC	300
	ACGAAACGAG ACTACAGCGA TGGGAGAGGT GGCATGAAGG CTTAGGGTGG GGATCGGTAG	360
15	GACCCATGCA CCCAGAGAAA GGGACTGGTG GCAACTTTCA AACTCTCTGG GGAAGGAAGA	420
	AGGGCTGAAA GAGGATGAAC GGGCTCAGGT ACTGCTCAAT GTGTGTGTGG CGGACCAAAG	480
	TGGGTATGGG GGCCCCGTAA GAGGGGCGGG GAAGGTGGAT AGGAAGGATC CCGGTAGACT	540
20	GGAGGGGATC CTGGAAAAGC ACCAGGGCTG CGAGCTAGGA ACCCATTGG AGTTAAGGGT	600
	ACAGGATCCC AGATGAGGGG GTGGGAAGCC TGGGACGGGC GGGACCAGAG AGGGAGGTCC	660
25	CACGGGCTGG TGGGGAAAGA GTGGGGGGCT TCGCGCAGGA GGATGGGACG TTCAGGAGTG	720
	GTAACTGGGC GGAGGCCGGC CGGGCGGGGC GCGCGGTGCC CGCGGGCGGT GGGAAAGGCCG	780
	GTGCGGGGCC CACGATCAAC CCCCCCCCAG GGGCCGGGCC GGGCCGGGGG CGGGGCCGGG	840
30	CGGGGCGAGC GGCGCATTAG CGCCTTGTCA ATTTCGGCTG CTCAGACTTG CTCCGGCCTT	900
	CGCTGTCCGC GCCCAGTGAC GCGCGTGAGG ACCCGAGCCC CAATCTGCAC CCCGCAGACT	960
35	CGCCCCCCGCC CCATAACCGGC GTTGCAGTCA CGGCCCGTTG CGCGCCACCC CCATGCCCGC	1020
	GGGTGCCCCG GGCCCCGTGCCC AATCCGC GCGCGGGGCC CGCGGGCCGC TGTCCCTCGCT	1080

	GTTGGTCGCCT	CTGTTGCTCT	GTGTCCTCGG	GGTGCCTCGG	GGCGGATCGG	GAGCCCGTGA	1140
	GTACCGTGCG	CCCTGCTCCC	CACCTCCCCA	GGGAAGCCGG	GATCCGGCGC	CCCGGGGGGT	1200
5	AGTCGCGGGG	GATGGAAGAA	GGGGCGCGAG	CGCCACCTGG	ACGTCCCAGG	AACAAAGGAA	1260
	GGCGGCCCTC	GGGGCGCCCT	CACCTGTGGG	GCTCATGGCA	CCACCACCCA	GCCTCCCAAG	1320
	AGTACCCCGT	TATAACATCAG	AGGCCTCTTA	TCTGTATCCC	CTTTGCGAGG	CTGTCTGGCC	1380
10	AGGCTCAGTT	TGAAGGACAT	CGCAGTGTCC	TGGGACCCCC	CTCCTTCAGG	GTGCTGGGAC	1440
	GCTTCGGGGC	GCACGCCTGT	GTCTGGATA	TCAGAGCGGA	AGGGAAGCCT	CCCTGGCCGG	1500
15	GGGCGCACGC	TTGGGTGCGT	TGGGTTGGGT	GCTGGCGCAA	AGTGGGGTCC	CCTCCCCCAT	1560
	GAAGTGATGA	TCCCCGGGGG	GAGGGTGGGG	CGTTATCGTG	AGCCCTCCTG	TCCGCCTGGC	1620
	ATGCGGGCCCG	GCGTCCCTCG	GGACTTGCCT	CTCCGTGGGG	TCGGCGCCGC	CCCCCTCCCC	1680
20	CTATAGCAGA	CTCCATGCTT	TGGTATCCTC	GAAGTCCTCT	CCACTGGTGG	GGCTCACAAAC	1740
	CGGTCTCATT	CAGGCTGCGC	TGGGTTGAGA	GCCTCTAGCG	ACTGAAATTT	CGGTGAGGAG	1800
25	CGAGAGCAAG	CGTGTCCGGG	CACCGCGAGC	CCAGACTTCA	TTGTCTAAGG	GGCACCCAGT	1860
	GGGGGTCAGC	TGCCGAGAGA	ATCCCACGT	CCCAGGAGGA	ACTCCTGGCC	TTGAGCCCC	1920
	ATCACCCAAAC	GCACACATCC	CCGCCAGGAT	GCGGTCTCCA	CATCCAGACC	CTCTCTGGGA	1980
30	CACACCCAAA	GACACACAAA	AGAGCCCCAC	TGGCTTATGT	CCC GTCA CCC	TGCCCTCCGA	2040
	CGCGCGCTGC	AGCCCAGATG	CGTATTGCA	CACCATCGCG	GCGCTCGCAT	TCCATCCTCT	2100
35	ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAC	ACACACAGAC	ACGCACACAC	2160
	ACACGCACGC	ACACACACGC	ACGCCCGCAC	TCGTGGTCCC	ACATTTATTT	CACAGGGAG	2220

	GCAACACCGG GGTACGCATA TGGTTGAGTG CACTGGAGAT CTTTCCCCAC CACTCTCAGG	2280
	ACCCCATCCG GAGACACAGG CCACACCGCA GGGGCACCAC GCTGCGCTGC TGCTCTGGC	2340
5	TAGTAGTCCT GTGCAGTTG TCCGCGGTGT CTGTGGACGC CCTCCCGCTC TTGTCAGGGG	2400
	ACAGGAACCT ACACTCCTGC TTGCCCAAGG CGGCTGGGCA GGTGATGTGG TGACACCCGG	2460
	GACCTTCCG GGGAGTTGGT GTTGCTGCCA AGCCTGGTA GTTTTGAAT GCCACCAATA	2520
10	GCGCTAAGCT TTGTTCCGG GCGGGCTGCA GAGAACAGG CGAAGGTGGC GGAGTGGGG	2580
	TGGCGCGTGT GTTTTTCTT TTAAGGGGA GAGAAATTAA ATAAGAGGTT CTCACACCTC	2640
15	TGCAATCTGT TTGTACTTAC CGTGTGTCTT AACACCTGAC CAGCCAGCCG GTGGGTCGTA	2700
	AAAGTGTATG CAGGTACCAAG CGGGACAGGA GATGGGGGCC CCTGGGTAT GGCTGGGATG	2760
	GAGGCCACCT TCCC GTTGGC CTTTCAGGGGA ATCTCACACT TTTCCCTTT AAAACACATG	2820
20	GTGTTCTTT TAATAACGGC AGCAACTCCG CATTGGAAA GGGGGAAATA AGCTTGTATA	2880
	GGCCCCGGCT TTGTGGAAAG GAGGGGAAGA GGGAGAAAA AAGGAGGGT GTCTCCTCCA	2940
25	GGCTTAGGGG GCTGTCAGCT GCTGCTCTGT CTAGCTTGGC ATGTGTGTGC CCCAGTCCCC	3000
	AGTGGCTTTG GCCCATTGTT TGTGGAAAGCC AAGAGGGAGA CTGGAGTCCT CTATCTCTGG	3060
	TACTCCAGAG TCAGGGCTTCT CAGTCCGAGC CCAGAGAACG TCTTCCCTGT TTTATGGAGG	3120
30	GAATCAGGGGA AGGGGGTGCC AGGTGGACTA CGTTCTGCTG AGGACTGTAC CAGTCGCTCG	3180
	AAGGAGAAAG CTTGGGCTTG CCCCCCTCCC CCCTCAAGCC ACGAAGGGCA GCTGCTAGGC	3240
35	TAGTGTGGTA AAAGGGCATT ACTCCCCAGC CAGGACCCCC CAGAGAGTCC CCTTCCTGGC	3300
	CAGACAAATG CTGGGGAGGG ACAGAGGGT GTGATCATTG CCCAGGAGTG CAGACAGTGG	3360

	GGTCCCGGGT CGGGCAGTGC CTCCCACCCCT GCTGAGGGGG GCGCCAGGC AGGAAGCGGT	3420
	GGGTGGGCCG GGGTAGAGAC GCTGGCACGT CCCAGTTCAT GCCGAAGGAA TTCTGAATT	3480
5	GCGGGCGGCT GGCTGCCTGG GACCTCCGGG GCGGGCCCCCT GGCCCCCGCC GCTCCGTCTG	3540
	GCCTGCTCCT CCTGCTCCTT CGCACGGACG CTGAGACCTC CGCTGAGCCC TGGGACAAGC	3600
	CCCAAATGCA ACTGCGATTG CAGGCTTCGC AAGACCCGCC TCCTCCCAAG GCCAAATTG	3660
10	CCTGGGAGAA GTCATTCAAGG GCCCAGACTA GAACCATGTT GGTGCCACCT CATCCATCTG	3720
	GGGCATGAAG GACCGTCCAG GGCTGCAGTT TAGCTTCTTA ATAGGAACCT GGGGGTGGGT	3780
15	GCAGCCTCTG TTCTCCGAGC CTCTTGAA ATCGTTTTG TTTTTGTTTT TGTTTTTCC	3840
	AATACTCTT TCCTCTCATC CCATCCCGGG ACTGTTTCC TCCCTAACGGG TTGAGAGCCC	3900
	TGCAGTCTTC CCTAACCTTT TCTTGCTTC TACCCCAGGG CCTTTGCACA TGGAGTCCA	3960
20	CCTCTCCCT TGCCCAACTG GGGCTCCAGC CTTACTGCAT TTGGCTCTTG GTAACTGTCC	4020
	CAGGGCCTCT CTGACACACA GGGTTGTAGC CCCAGCTCCC TCTTTCTCC TCCCCCCTTT	4080
25	CTCTTTGCT TCTGAGACTT AATTTTTTC TTTTTCTTTT TGGCTTTTG AGACAGGGTT	4140
	TCTCTGTACA GCCCTGGCTG CCCTGGCACT CATTCTGTAG ACCAGGCTAG CCTCAAACTC	4200
	ACAAACCTAC CTGCCTCTGC CTTCCAGTG CTGGCACTAA AGATGTGGGC CACCACAACT	4260
30	AGTAGTTAAG TGTTTGCTG TGTCTTTATT CCTATAGTGA CCTCAGTTCC TGGCATATTG	4320
	TAGGCGATGG ATGGATGAAT GGATGGATGG ATGGATGGAT GGATGGTTGG ATGGAGCAAG	4380
35	CTTGAATCGT CCTGAGTGAA AAAAGAGACC TCAGAGAACT GAATGGAGTT AGGTTCCAG	4440
	GGCAGCCTGG CCTGCTGGTC TCATGGGAGC TCCCTGTGAA ACTTCCCCCA CACCTCCCAC	4500

	CACCCCTGCCA TCCTGTGTGG CTGACAAGAA AGGCCAATGG CCAGATGGGG ACACAGACTC	4560
	AGGAAAGCTT GGAATATGTT CCCCTCCTCA TATCCTAGGC CTTGTTGTCC CCCTGAGGGC	4620
5	CCAGCCTATG AGTAGGGCAG CTGTGGGCTG CCCTAAGGTT GGGTAGGCAA GAAGGGGTG	4680
	GTCCCTCAGG GTGGGTACACA GGATTGAGGT CATTTCACAA GTGGCCATCA CAGTGGCCCT	4740
	AGGAAATGAT TGTGGAGAGT CAGAACTCCT GTTGGAGTT GTAGAGGGCC TTGCATGTGG	4800
10	GCTTCTGTGG CTGTCCCTTC TCTTGTGGTC CTTTGCACAG TCCCCTCGTG TGTGCTGGGA	4860
	TGTGAGGAGG GCACGGGAA AATGAAGGCT CAGCCCCCTCA GCTTGCCCTT CACGGTTCAC	4920
15	CCAACAGGGC TCACCTCTCC TCTGGACAGG CTCTCACTGT ATGCACAGAT TGGCCTCAC	4980
	TTTGATTCCC TTCCTTGGT CTCCTGGAT GACAAACATT TACCAGGGTA GGATTTACA	5040
	TTTTAGATAT GTCCATTCTC CAGAAACACA CTTGTGAGGT TAGGGTATCA GTGAAAGGAC	5100
20	ACCACCAGGA CAGACAAAGA ATTGGAGAGG AAGGAAATTG GTAAGCCAGG CCATGCTTGA	5160
	TGGCTTATGT GTAATCCCAG AACTCTGGAC GCTGAGGCAG GAGGATTCCA AGTTTCAAGA	5220
25	CAGTGTGTTTC TAGGTAATGA GACCCTGTCA AGAAAAGAAA AGAAATAAAG AGACAAGAAA	5280
	ATGTTTATAG GCTGTGAGAC AGCTTGGTGG GTAAGGGCA CTTGCCTCCA ATCAAGATGA	5340
	CCTCAGCCCC ATCCCTAGGA ATCCATGGTA GAAGGGAGAAA GCAAACCTCCA GCTGCTGACC	5400
30	TCCATACATG TGCTCCAATG TGCACACACA CAGGGAGACA TAATCAATTAA ATAGGATGTA	5460
	TTTGCTTAGA TTTGAGTAGG CATTATGAC TGATGTTTTA AAATTTTTAT TTGATTTAT	5520
35	GAAAATATAAC CTGTTGTAT TTGGTTGGT TTGGTTTGAG TTTTGTAT TTGAGACAGG	5580
	GCTTCTCTGT GTAGTCCTGG CTGTCCCTGG AACTCACTCT GTAGACCAGG CTGGCCTTGA	5640

	ACTCAGAAAT CCGCCTGCTT GTGCTTCCA AGTGCTTAGA TTAAAGGTGT GCACTGCCAT	5700
	TCAGCAAAAT TGCATACTTT AACCCCAGTA TTTGGGAGGC AGAGGCAGAC TAATGTGTGA	5760
5	ATTCCAGGCT AGCCAAGGAT ACAGAGTGAG ACCCTATTCT TACCTCTCCC CCCCCAAAACC	5820
	CCAAAATGTA TTTTGTGCTT GTGTATGTAC ATGTGTGTTG CAGCACGTAA ATGTCCAAGG	5880
	ACAACTTGTA GAAGTTCTCT CCGTTCACAG TCTAAGTCCT GAATTCAAAC TAAGGTCCCTC	5940
10	AGGCTTAGCC ACAGTCTTCT TTATGTACTG AGCCATTCA CTGGCCCTGG ATTGACTGAT	6000
	GAATTAATTT TTGAGATAAG GTCTCTTGT A GCTCTAGCTA GGCTCAAAC ATGAACCTCCC	6060
15	AAGGTCATCT TGAGCTGCTG GTACTCTTGC TTCCACCCCA AGTGGTGGAA TGATACTCAG	6120
	GCAGCACTTC TCTGGGGAAG GGGCTGGCCT TGGCCTTGAT TTTGTTGCCT CAGCTTCAAT	6180
	GAGTGCTTGG GTCTCGTTGT TTCTTTCTT TATCTGTGAA ATGGGTGAAC ACCTGTTCAA	6240
20	GACTTCCTGA CTCTTGAAAC ATCCAGGCAG GGTGAGGGAC TTGAAGTGGG CTCATCCCAT	6300
	GCCTAACAAA GTGTCGTCTT TGACCCCAGA CACAGCTGTA ATCAGCCCCC AGGACCCAC	6360
25	CCTTCTCATC GGCTCCTCCC TGCAAGCTAC CTGCTCTATA CATGGAGACA CACCTGGGGC	6420
	CACCGCTGAG GGGCTCTACT GGACCTTCAA TGGTCGCCGC CTGCCCTCTG AGCTGTCCCG	6480
	CCTCCTTAAC ACCTCCACCC TGGCCCTGGC CCTGGCTAAC CTTAATGGGT CCAGGCAGCA	6540
30	GTCAGGAGAC AATCTGGTGT GTCACGCCCG AGACGGCAGC ATTCTGGCTG GCTCCTGCCT	6600
	CTATGTTGGC TGTAAGTGGG GCCCCAGACA CTCAGAGATA GATGGGGTT GGCAATGACA	6660
35	GATTTAGAGC CTGGGTCTTC TGTCCCTGGG CAGAGCCATG GGCTCTCACT TGCATGCAGG	6720
	CATGGTCATA CCCAGCACAG GCATTGCAAC TCTAGGGACA GCTGTGGCTG CACTGTCCCC	6780

	TGTGTACCCC ACAGCTTAG AAAAGCTGTC ATGTTTCCCT TGTAGTGCCC CCTGAGAAGC	6840
	CCTTTAACAT CAGCTGCTGG TCCCGGAACA TGAAGGATCT CACGTGCCGC TGGACACCGG	6900
5	GTGCACACGG GGAGACATTG TTACATACCA ACTACTCCCT CAAGTACAAG CTGAGGTTGG	6960
	TACCCAGCCA AGCCTTGCTG TGTGACTTCT GGCAATACTT ACCTTCTCTG ATCAAATATG	7020
	TTCCTGTTA TGAACTCAAA AGGGACTCTC GCACCTCCAC AGGTGGTACG GTCAGGATAA	7080
10	CACATGTGAG GAGTACCACA CTGTGGGCC TCACTCATGC CATATCCCCA AGGACCTGGC	7140
	CCTCTTCACT CCCTATGAGA TCTGGGTGGA AGCCACCAAT CGCCTAGGCT CAGCAAGATC	7200
15	TGATGTCCTC ACACTGGATG TCCTGGACGT GGGTGAGCCC CCAGTGTCCA CCTGTGTTCT	7260
	GCCCTAGACC TTATAGGGCG CCTCCCCCCC ATCCCCCCAG ACTTTTGTT TCTTCTAGAG	7320
	GTCTTAGCCA CAGCCACGGT GGTTGCAGGA CAGTGGTTGT TCATAACTTA ATGCAAAGAC	7380
20	TTTCCCCCAA GACAGTCAAG ATTTTCCCT CCCACCCCC AACACACACA TACACACACA	7440
	CTCTGCAGAG AACACCTGGC CTGACCACCC TCCCTCTCTA CAGCCCAGGT GTTCAGAAGG	7500
25	GAGTCCTAGG GGACTGAGAG GAGGCGCCCA GGTCTGAAGG CGCCCCAGGA AGCCGAGGCC	7560
	TTGAGCTGGG GGGGGGGGGCG AGGGTTGGAG GCACGAACTG GATGATCCCT GAGCACAACT	7620
	GGGCCTAATC TAATTAGGGT GTTCCCAGCC CAAAGCAGCC TGGGCCATT AACCCTTCAA	7680
30	GTGCCTCACT GAAGACTCAG GGGAGAGATC AGCTTGTACT CTCTCCATGG TCCCCCAGGA	7740
	GGGTTCTGG GTGCCCTGG CTCATTCCCA CATCCAGAGG TTTTGTGTCT TCCTGGCCTC	7800
35	TAACCCTCAG TTGTGCTCTG TGGCTGGCAC AGCTGCCCCG TGGAGGCTCT TGGTAATGTA	7860
	CAAGGCATCA GAGGTGGACA TGGGATGGGG ATACATAGGG ATGGAGCCAA ATAGCACCTC	7920

	AAGGTGGGGT GATATACAAT AAAGCTTGTC ACCCTGACGC TCAGAAAGCC TACTCATGAT	7980
	GATCACAAATT GTTGACATCA CTCTGGGACA TGTAGTGAGA CCCTAGCTCA AAACACAGAC	8040
5	AGTAGCTTTA AGAGTCAGCT TGTGACTTAA TACTGGAACT CAGGGCCTAA TAGGTGCTGG	8100
	GTGATGCTCG CCTCACTCCC TGTTTAGTGA GATCTCTGCG CTAATCTCCA CCCCCAGCTGG	8160
	GTGGGCTGCT CTGTCCCCCTT GAGGGCAGGA ATGTGTGTCT TCCATCAGAG ATAGGACCCG	8220
10	TGGTAGCAGC AACTGCTGCT GGCTGTTCT GGAATATTAA ATGACAGTAA TCTATCAGGC	8280
	CTGGGTGAGT AGCTAACAGG GGTGGGGCG TGGTCTGGAA AACGCAGATA GGGTCATAGG	8340
15	AGCCACTGCA GCCTAGATTA CACCACTGGG TGTTCTGTCA CTAGGCCATT CTCACCAAGC	8400
	AGTCCTCAGA ACTGGGAGCA CTGTTGCCAG CATTAAATGC CAGCATTAA TGCCAGCATT	8460
	AGGGGAGGCA GAGGCAGAAG GATCTCTCTG AGTTCAAGGC CATCCTGAAT TTACATAAAG	8520
20	AGCTCCAGGC CAGCCAGGGT GCGCAGTAAA ACCTTGTCTC AAAAAACAAA GCATCTTAG	8580
	TGACCAGGCT TGCTCCACCC CCAGTGACCA CGGACCCCCC ACCCGACGTG CACGTGAGCC	8640
25	GCGTTGGGGG CCTGGAGGAC CAGCTGAGTG TGCGCTGGGT CTCACCACCA GCTCTCAAGG	8700
	ATTTCCTCTT CCAAGCCAAG TACCAAGATCC GCTACCGCGT GGAGGGACAGC GTGGACTGGA	8760
	AGGTGCCCGT CCCGCCCCGG ACCCGCCCCCT GACCCCGCCC CCCGCATCTG ACTCCTCCCT	8820
30	CACCGTGCAG GTGGTGGATG ACGTCAGCAA CCAGACCTCC TGCCGTCTCG CGGGCCTGAA	8880
	GCCCCGGCACC GTTTACTTCG TCCAAGTGCG TTGTAACCCA TTCGGGATCT ATGGGTGAA	8940
35	AAAGGCGGGA ATCTGGAGCG AGTGGAGCCA CCCCACCGCT GCCTCCACCC CTCGAAGTGG	9000
	TGAGCACCTC TCCAGGGCTG GCTGGCCCAT GGAATCCCCA ATCCATCCTG TTCCCTCCCC	9060

	CCCACCCCTT TTTTGAGACA GCGTCTTCAG GTAGCGCATG CTGGCCTTAA ATTCA GTATG	9120
	TAGTCAAGGA TGACCTCGAG CTCCTGGTCT TTTGTCTCC ACTTAGAGAC AATGCCAGT	9180
5	GGCCATCACCC ACCTTGGGA GACTAGCCAT GGAGTCTATT TAGCCTGTCA TTTGGTGACA	9240
	GATGGAGTAC AACAGTGTGA CCTCTTGTAA GAGAACTGAA GACAGGCTGT TTTTAACCCC	9300
	AATATCCTAG GCTCTCTAGA GTTAACTTT ATATAAAATA GAGACTATTA CAGCCAGTTA	9360
10	TCACATGGTC CCACAGAACCC TTGTCACA CAACCTATAG ACCACAGTGC CTGTGCCTAC	9420
	CACATAAGGG TCTCTACTGC TGGCCCACCC CTCCAACCCCT TAAAAGGTAA CCTAGGCAGC	9480
15	CTTAATATTT GCAATCCTCC TACCTCAGCC TCTTGAATGC TCAGAAACCA GGCA TTAAACC	9540
	CAAGTTTCTC TTCTCTGGT CCCTTTCTTA AGGTGGGAGG GCCTAAAGAT GACTTCCTTT	9600
	GTCCTGAAGA CTCTCCGAGC CCATGGATCT GCACTCTCTA ATATGAAATA TATTGCATAA	9660
20	AATGTCTGGC CTCAGTTCC CCACCTGTCA GGTTAGGCA GCACAGTCGG TCCAAGACAC	9720
	TTCATTATTT GCAGGCAGTA TAAGAAGAAG CTCCCATCCC CCACCCGCTT CCTCCGGTCC	9780
25	CTAAGACAGA ATACTTCTAC ACTGAAACTG AACTCTCGCA GACGCATATG CTCACTTTAA	9840
	TGATGATGAA ATAATGGGAA AACTGAGGCT CCGAGAGATT CCTGGAGGAA GAGGGTCAA	9900
	ACCAGCTCCA GGAAGCTCTC CAGCCCCAT CCGGGCCTCT CCAGGTTCTG GGCTTGGCGG	9960
30	GAGTGAACAC AGCTGGGAGG GGCTGGAGCC TGGGAGCTTT GGCCCTTGCT CGTGCCAGC	10020
	ACCTGCGATT CTTGCACGGG AGCCAGCAGG CGGCTGCGTC CGCCCCAGAG ACTGAAGAAG	10080
35	CCGGGGGTAG GGTTGGAGGG AGGTAAGCAG GGGCTGTGGG GGCCGAAGCT TGTGCCAGGG	10140
	CCTGTCAGCG AGTCCCCAGT TTTATTTATG GCGTGAGGCC GATGTCTTAA TCCGCTGGCC	10200

	TGCTGGGGGA TGGCTGCAGC TGGGGATTGG ACCCAAGGGC TGGCTTCCCA CTCAGTCCTC	10260
	CAGCCCACTC CATGTACACAC CGTGCAATTC TCTGAGGCTT ATCTTGGAA CCCGCCCTTG	10320
5	TTCTGTGCTG TCTGTCTCTA TTTCTGTCTAT TCACCTTCCC AGAGCCTTTT TTTTATGCTT	10380
	TTAATATAAAC TACGTTTTAA AAATTGCTTT TGTATAATGT GTGTGCCTTC GTGAGCGTGC	10440
	GTGCCACAAC ACACACGTGA AGGTTAGAGA ACTTTGTTGA GTAGGCTCCT TCCACCATGT	10500
10	GGGACTAGGG CTGGCGACAA GAGCAATTAC TGAGTCATCT CGCCAGCCCC TCACCCCTCA	10560
	CTTCCCACATCC TGTTTGGATA GTCATAGGTA ATCGAAGGTA AATCGCTGGC TTTAATTCG	10620
15	TAGCTATCCT GCCTCAGCCT ACCAAGTGCT GTGCTACACAC GTTTGTGGGA GGGGCTCTCC	10680
	TCCCAGTGTC TGGGGGTACA CAGTCCAAG ATCTCTGCTT TCTAGGTCTT TGTCTTAGTT	10740
	TGCCCCTTGC TTTGTCCGTG TCCCTAGAGT CTCCGGCCCC ACTTAGTCTC CATTGATTTC	10800
20	CTTTCTGACC GAATACTCGG TTTTACCTCC CACTGATTTG ACTCCCTCCT TTGCTTGTCT	10860
	CCATCGCCGT GGCATTGCCA TTCCCTCTGGG TGACTCTGGG TCCACACCTG ACACCTTCC	10920
25	CAACTTTCCC CAGCCGAAGC TGGTCTGGTA TGGGAGGCCG CCGTCCCGCG CGCGCCTCCT	10980
	GCTGGCCCGCG CCCCAACACT GCCGCTCCAT TCTCTTACA GCGCCCGGGC CGGGGCGGCG	11040
	GGGTGTGCGA GCCGCGGGGC GGCGAGCCCA GCTCGGGCCC GGTGCGGCGC GAGCTCAAGC	11100
30	AGTTCCCTCGG CTGGCTCAAG AAGCACGCAT ACTGCTCGAA CCTTAGTTTC CGCCTGTACG	11160
	ACCAAGTGGCG TGCTTGGATG CAGAAGTCAC ACAAGACCCG AAACCAGGTA GGAAAGTTGG	11220
35	GGGAGGCTTG CGTGGGGGGT AAAGGAGCAG AGGAAGAGAG AGACCCGGGT GAGCAGCCTC	11280
	CACAAACACCG CACTCTTCTT TCCAAGCACA GGACGAGGGG ATCCTGCCCT CGGGCAGACG	11340

GGGTGCGGCC AGAGGTAAGG GGGTCTGGGT GAGTGGGCC TACAGCAGTC TAGATGAGGC 11400

CCTTTCCCT CCTTCGGTGT TGCTCAAAGG GATCTCTTAG TGCTCATTTA ACCCACTGCA 11460

5 AAGAGCCCCA GGTTTACTG CATCATCAAG TTGCTGAAGG GTCCAGGCTT AATGTGGCCT 11520

CTTTCTGCC CTCAGGTCTT GCCGGCTAAA CTCTAAGGAT AGGCCATCCT CCTGCTGGGT 11580

CAGACCTGGA GGCTCACCTG AATTGGAGCC CCTCTGTACC ATCTGGCAA CAAAGAAACC 11640
10 TACCAAGAGGC TGGGCACAAT GAGCTCCCAC AACCAACAGCT TTGGTCCACA TGATGGTCAC 11700

ACTTGGATAT ACCCCAGTGT GGGTAGGGTT GGGGTATTGC AGGGCCTCCC AAGAGTCTCT 11760

15 TAAATAAAAT AAAGGAGTTG TTCAGGTCCC GATGGCCAGT GTGTTGGGG CCTATGTGCT 11820

GGGGTGGGGG GA 11832

20 (2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
(B) TYPE: amino acids
25 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

35 Val Ile Ser Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser

5

10

15

20

Ile His Gly Asp Thr Pro

25

- 131 -

SUBSTITUTE SHEET (RULE 26)

CLAIMS:

1. A nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a novel haemopoietin receptor or derivative thereof having the motif:

Trp Ser Xaa Trp Ser [SEQ ID NO:1],

10 wherein Xaa is any amino acid.

2. A nucleic acid molecule according to claim 1 wherein Xaa is Asp or Glu.

15 3. A nucleic acid molecule according to claim 1 or 2 wherein said nucleic acid molecule is capable of hybridisation under low stringency conditions at 42°C to:

5N (A/G)CTCCA(A/G)TC(A/G)CTCCA 3N [SEQ ID NO:7]; and

20 5N (A/G)CTCCA(C/T)TC(A/G)CTCCA 3N [SEQ ID NO:8].

4. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:12 or a nucleotide sequence having at least 60% similarity 25 to the nucleotide sequence set forth in SEQ ID NO:12 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42°C.

5. A nucleic acid molecule according to claim 3 comprising a 30 sequence of nucleotides substantially as set forth in SEQ ID NO:14 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:14 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42°C.

35

6. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID

NO:16 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:16 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 421C.

5

7. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:18 or 24 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:18 or 24 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 421C.

8. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:28 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:28 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 421C.

9. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:38 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 421C.

10. A nucleic acid molecule according to claim 4 or 5 or 6 or 7 or 8 or 9 wherein said haemopoietin receptor is of murine origin.

30

11. A nucleic acid molecule according to claim 9 wherein said haemopoietin receptor is of human origin.

12. An expression vector comprising a nucleic acid molecule selected from the list consisting of:
(i) a nucleotide sequence as set forth in SEQ ID NO:12;
(ii) a nucleotide sequence as set forth in SEQ ID NO:14;

- (iii) a nucleotide sequence as set forth in SEQ ID NO:16;
- (iv) a nucleotide sequence as set forth in SEQ ID NO:18;
- (v) a nucleotide sequence as set forth in SEQ ID NO:24;
- (vi) a nucleotide sequence as set forth in SEQ ID NO:28; and
- 5 (vii) a nucleotide sequence as set forth in SEQ ID NO:38.

13. A method for cloning a nucleotide sequence encoding a haemopoietin receptor having the characteristics of NR6 or a derivative thereof, said method comprising searching a nucleotide database for a sequence which encodes an amino acid sequence as set forth in one or more of SEQ ID NO:1, SEQ ID NO:7 and/or SEQ ID NO:8, designing one or more oligonucleotide primers based on the nucleotide sequence located in said search, screening a nucleic acid library with said one or more oligonucleotides and obtaining a clone therefore which encodes NR6 or a part or derivative thereof.

14. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:13 or having at least about 50% similarity thereto.

15. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:15 or having at least about 50% similarity thereto.

30 16. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:17 or having at least about 50% similarity thereto.

35

17. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative

thereof having an amino acid sequence substantially as set forth in SEQ ID NO:19 or having at least about 50% similarity thereto.

5 18. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:25 or having at least about 50% similarity thereto.

10

19.. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:29 or having at least about 50% similarity thereto.

15

20. An isolated novel haemopoietin receptor comprising the amino acid motif:

20

Trp Ser Xaa Trp Ser [SEQ ID NO:1]

wherein Xaa is any amino acid.

25

21. An isolated haemopoietin receptor according to claim 20 wherein Xaa is Asp or Glu.

22. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:13.

30

23. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:15.

35

24. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:17.

25. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:19.

5 26. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:25.

10 27. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:29.

15 28. A method for modulating expression of NR6 in a mammal, said method comprising contacting a genetic sequence encoding said NR6 with an effective amount of a modulator of NR6 expression for a time and under conditions sufficient to up-regulate or down-regulate or otherwise modulate expression of NR6, wherein the genetic sequence encoding said NR6 is selected from the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 20 16 or 18 or 24 or 28 or 38 or is a sequence having at least about 60% similarity to at least one of SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 and is capable of hybridising thereto under low stringency conditions at 42°C.

25 29. A method of modulating activity of NR6 in a mammal, said method comprising administering to said mammal, a modulating effective amount of a molecule for a time and under conditions sufficient to increase or decrease NR6 activity wherein said NR6 comprises an amino acid sequence:

30 (i) encoded by a nucleotide sequence selected from the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 and which is capable of hybridising thereto under low stringency conditions at 42°C; and

(ii) substantially as set forth in SEQ ID NO:12 or 14 or 16 or 18 or 32 or 30 or a sequence having at least 50% similarity thereto.

5 30. A pharmaceutical composition comprising an NR6 receptor in soluble form and one or more pharmaceutically acceptable carriers and/or diluents wherein said NR6 comprises the amino acid sequence:

10 (i) encoded by a nucleotide sequence selected from the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 and which is capable of hybridising thereto under low stringency conditions at 42°C; and
15 (ii) substantially as set forth in SEQ ID NO:12 or 14 or 16 or 18 or 32 or 30 or a sequence having at least 50% similarity thereto.

20 31. An isolated antibody or a preparation of antibodies to an NR6 receptor, said NR6 receptor comprising the amino acid sequence:

25 (i) encoded by a nucleotide sequence selected from the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 and which is capable of hybridising thereto under low stringency conditions at 42°C; and
30 (ii) substantially as set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 or a sequence having at least 50% similarity thereto.

35 32. A transgenic animal comprising a mutation in at least one allele of the gene encoding NR6.

33. A transgenic animal according to claim 33 comprising a mutation in two alleles of the gene encoding NR6.

34. A transgenic animal according to claim 33 or 34 wherein
5 said animal is a murine animal.

1/43

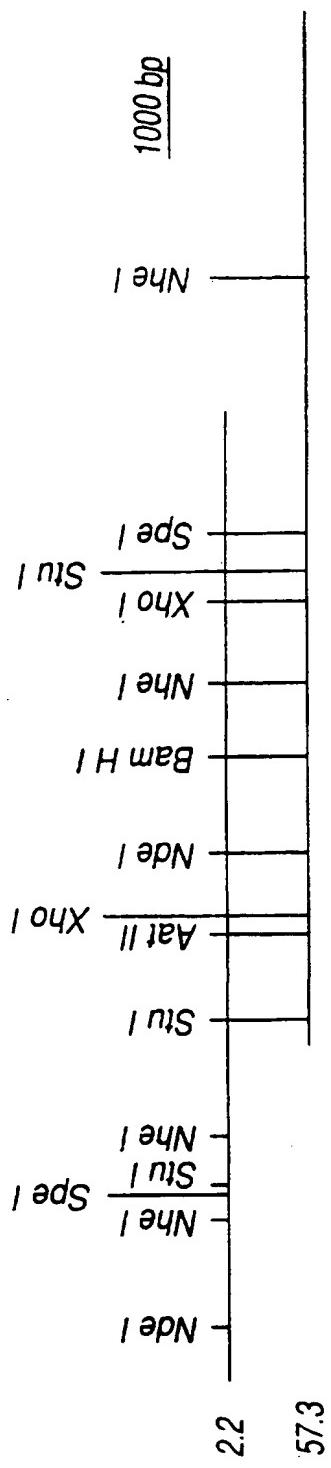
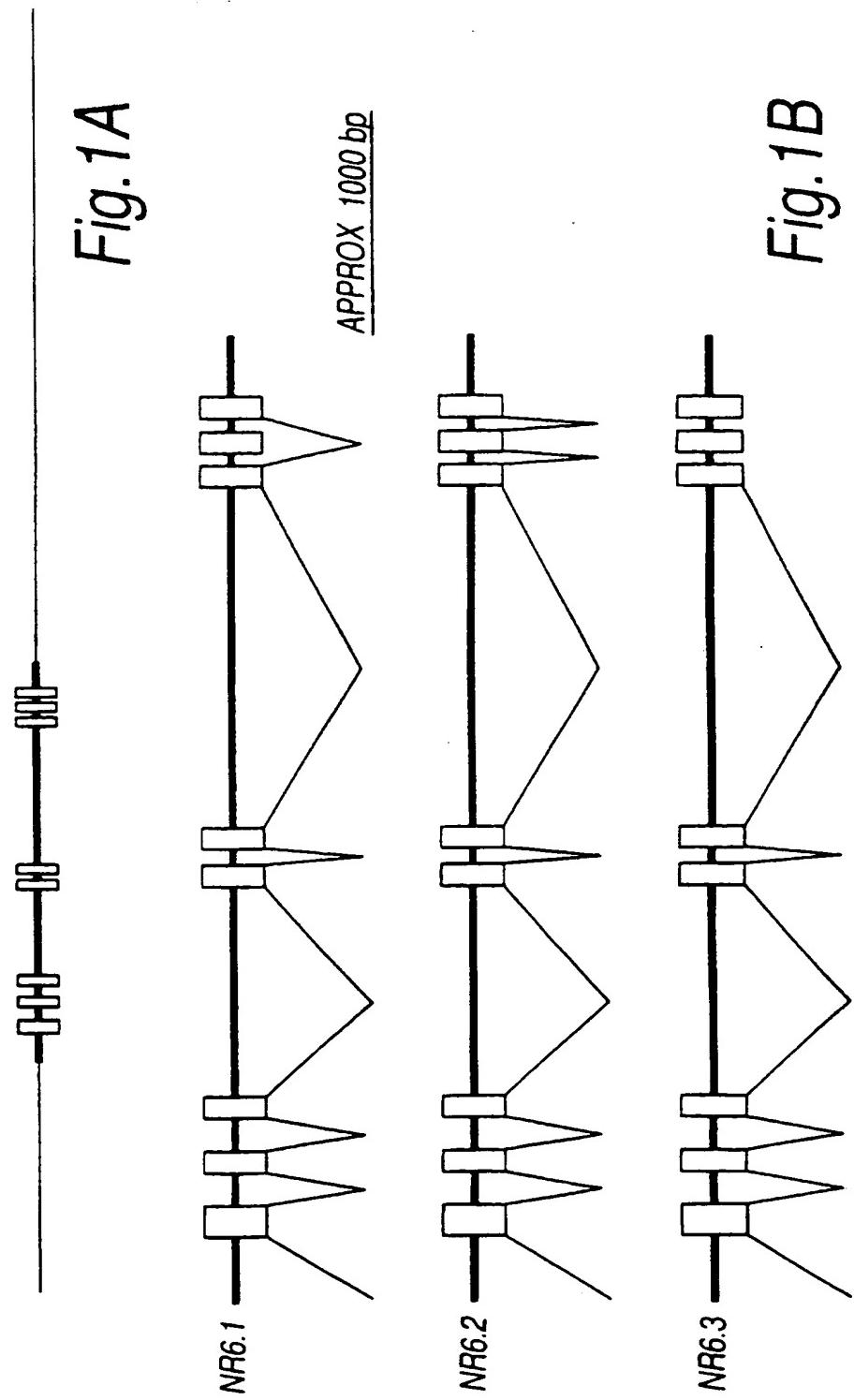


Fig. 1A



2/43

3/43	4/43
5/43	6/43
7/43	8/43
9/43	10/43
11/43	12/43
13/43	14/43
15/43	16/43
17/43	18/43

Fig.2

3/43

g1	cccaagaactct
g38	agtttcaagacagtggtt
g83	aagaaaaagaaaataaaagaga
g128	cagcttggtggtaagggg
g173	agccccatcccttaggaatc
g218	cagctgctgacacctccatac
g263	ggagacataatcaattat
g308	ggcatttatgactgatgtt
g353	aatataacctgtttgtattt
g398	atttgagacagggcttc
g443	tcactctgttagaccaggct
g488	tttgtgcttcccaagtgc
g533	gcaaaattgcataactttaa
g578	actaatgtgtgaattccag
g623	ctattcttaccctcccccc
g668	tttgttatgtacatgtgtg
g713	actttagaagttctctcc
g758	actaaggcctcaggctta
g803	catttcactggccctggat
g848	aggctctttgttagctctag
g893	gtcatctttagctgctgg
g938	aatgataactcaggcagcac
g983	ccttgattttgttgcctca
g1028	gtttctttctttatctgt
g1073	ttcctgactcttgaaacat

Fig.2(i)

4/43

tggacgctgaggcaggaggatccca
tctaggtaatgagaccctgtcaagaa
caagaaaatgtttataggctgtgaga
cacttgccctccaatcaagatgacctc
catggtagaaggagaaagcaaactcg
atgtgctccaatgtgcacacacacag
agatgtatttgcttagatttgagta
ttaaaaattttatttgatttatgaa
ggtttggtttggtttagttttgttt
tgtgttagtcctggctgtccttggAAC
ggccttgaactcagaaatccgcctgc
agattaaagggtgtgcactgccattca
ccccagttttgggaggcagaggcag
gctagccaaggatacagagtgagacc
ccaaaacccaaaaatgtatttgatgc
ttgcagcacgtaaatgtccaaaggaca
gttcacagtctaagtcctgaattcaa
gccacagtcttctttatgtactgagc
tgactgatgaattaattttgagata
ctaggctcaaactatgaactcccaag
actcttgcttccaccccaagtggtgg
ttctctggggaaaggggctggccttgg
gcttcaatgagtgcttgggtctcggt
gaaatgggtgaacacacctgttcaagac
ccaggcagggtgaggacttgaagtg

Fig.2(ii)

5/43

g1118	ggctcatccatgcctaac
g1163	agctgtaatcagcccccaag
g1208	L Q A T C S <u>CCTGCAAGCTACCTGCTCT</u>
g1253	A E G L Y W <u>CGCTGAGGGGCTCTACTGG</u>
g1298	E L S R L L <u>TGAGCTGTCCCGCCTCCCTT</u>
g1343	A N L N G S <u>GGCTAACCTTAATGGGTCC</u>
g1388	C H A R D G <u>GTGTCACGCCGAGACGGC</u> V G
g1433	<u>TGTTGGCTgttaagtggggc</u>
g1478	ttggcaatgacagatttag
g1523	agccatgggctctcaacttg
g1568	aggcattgcaactctaggg
g1613	gtaccccacagctttagaa

Fig.2(iii)

6/43

aaagtgtcgctttgaccggagacac
D P T L L I G S S
GACCCACCCTCTCATCGGCTCCTC

I H G D T P G A T
ATACATGGAGACACACCTGGGGCCAC

T F N G R R L P S
ACCTTCAATGGTCGCCGCCTGCCCTC

N T S T L A L A L
AACACCTCCACCCTGGCCCTGGCCCT

R Q Q S G D N L V
AGGCAGCAGTCAGGAGACAATCTGGT

S I L A G S C L Y
AGCATTCTGGCTGGCTCCTGCCTCTA

cccagacactcagagatagatggggg

agcctgggtcttctgtcctggggcag
catgcaggcatggtcataaccagcac
acagctgtggctgcactgtcccctgt

L
aagctgtcatgtttccttgttagTGC

Fig.2(iv)

SUBSTITUTE SHEET (RULE 26)

7/43

	P	P	E	K	P	F	N
g1658				<u>CCCCTGAGAAGCCCTTAA</u>			
g1703	K	D	L	T	C	R	W
				<u>AGGATCTCACGTGCCGCTG</u>			
g1748	F	L	H	T	N	Y	S
g1793				<u>TCTTACATACCAACTACTC</u>			
g1838	ccagccaaggccttgctgtg						
	tgatcaaataatgttccctgt						
g1883					W	Y	G
	cctccacag <u>GTGGTACGGT</u>						
g1928	T	V	G	P	H	S	
				<u>CACTGTGGGCCCTCACTCA</u>			
g1973	F	T	P	Y	E	I	
				<u>CTTCACTCCCTATGAGATC</u>			
g2018	S	A	R	S	D	V	
				<u>CTCAGCAAGATCTGATGTC</u>			
g2063	tgagccccccagtgccacc						
g2108	cgcctccccccatcccccc						
g2153	ttagccacagccacgggtgg						
g2198	taatgcaaaagactttcccc						

Fig.2(v)

8/43

I S C W S R N M
CATCAGCTGCTGGTCCC GGAAACATGA

T P G A H G E T
GACACC GG GTGCACACGGGGAGACAT

L K Y K L R
CCTCAAGTACAAGCTGAGgttggta
 tgacttctggcaataacttacaccttc
 ttatgaactcaaaaagggactctcgca

Q D N T C E E Y H
CAGGATAAACACATGTGAGGGAGTACCA

C H I P K D L A L
TGCCATATCCCCAAGGACCTGGCCCT

W V E A T N R L G
TGGGTGGAAGCCACCAATCGCCTAGG

L T L D V L D V
CTCACACTGGATGT CCTGGACGTGGg

tgtgttctgccctagacacctataggg
 cagactttttggttcttagaggc
 ttgcaggacagtggttgttcataact
 caagacagtcaagattttccccctcc

Fig.2(vi)

9/43

g2243	ccacccccaacacacacat
g2288	ggcctgaccaccctccctc
g2333	gtccttagggactgagagg
g2378	ggaagccgaggccttgagc
g2423	acgaactggatgatccctg
g2468	ggtgttcccagccccaaagc
g2513	gcctcaactgaagactcagg
g2558	tggtcccccaggagggttc
g2603	tccagagggtttgtgtctt
g2648	ctgtggctggcacagctgc
g2693	aggcatcagaggtggacat
g2738	caaatacgacacctcaaggtg
g2783	cctgacgctcagaaagcct
g2828	tcactctgggacatgtagt
g2873	tagcttaagagtcagctt
g2918	taataggtgctgggtgatg
g2963	tctctgcgctaattccac
g3008	cttggggcaggaatgtgt
g3053	gtacgacaactgctgctg
g3098	taatctatcaggcctgggt
g3143	gtctggaaaacgcagatag
g3188	ttacaccactgggtgttct
g3233	tcctcagaactgggagcac
g3278	taatgccagcattagggga
g3323	ttcaaggccatcctgaatt
g3368	ggtgcgcaagtaaaaccttg

Fig.2(vii)

10/43

acacacacactctgcagagaacac
tctacagcccaggtgttcagaaggga
aggcgcccaggtctgaaggcgcccc
tggggggggggggcgaggggtggaggc
agcacaactgggcctaattcaattag
agcctgggccatttaacccttcaagt
ggagagatcagcttgtactctctcca
ctgggtgcccctggctcattccaca
cctggcatctaaccctcagttgtgct
cccggtggaggctttggtaatgtaca
gggatggggatacatagggatggagc
gggtgatatacaataaaagcttgcac
actcatgatgatcacaattgttgaca
gagaccctagctaaaaacacagacag
gtgacttaataactggactcagggcc
ctcgccctcactccctgttagtgaga
cccgctgggtggctgctctgtccc
gtcttccatcagagataggaccctg
gctgtttctggaatattaaatgacag
gagtagctaacaggggtggggcgctg
ggtcataggagccactgcagcctaga
gtcacttaggccattctcaccaagcag
tgttgcagcatttaatgccagcatt
ggcagaggcagaaggatctcttgag
tacataaaagagctccaggccagccag
tctcaaaaaacaaagcatcttagtg

Fig.2(viii)

11/43

g 3 4 1 3	accaggcttgc tccacccc
g 3 4 5 8	V H V S R V G GTGCACGTGAGCCGCGTTG
g 3 5 0 3	R W V S P P CGCTGGGTCTCACCA C C A G
g 3 5 4 8	K Y Q I R Y <u>AAGTACCAGATCCGCTACC</u>
g 3 5 9 3	gtgcccgtcccgccccggaa
g 3 6 3 8	ctgactcctccctcac cgt
g 3 6 8 3	Q T S C R L A <u>AGACCTCCTGCCGTCTCGC</u>
g 3 7 2 8	F V Q V R C N <u>TCGTCCAAGTGCGTTGTAA</u>
g 3 7 7 3	K A G I W S E AGGCGGGAAATCTGGAGCGA
g 3 8 1 8	T P R S <u>CCCCTCGAACAGTGgtgagca</u>
g 3 8 6 3	aatccccaaatccatcctgt

Fig.2(ix)

SUBSTITUTE SHEET (RULE 26)

12/43

V	T	T	D	P	P	P	D	
cagTGACCACGGACCCCCCACCCGAC								
G	L	E	D	Q	L	S	V	
GGGGCCTGGAGGACCGAGCTGAGTGTg								
A	L	K	D	F	L	F	Q	A
CTCTCAAGGATTCCTCTTCCAAGCC								
R	V	E	D	S	V	D	W	K
GCGTGGAGGACAGCGTGGACTGGAAG								
cccgcccctgaccccgccccccgcat								
V	V	D	D	V	S	N		
gcag <u>GTGGTGGATGACGTCAGCAAACC</u>								
G	L	K	P	G	T	V	Y	
<u>GGGCCTGAAGCCGGCACCGTTACT</u>								
P	F	G	I	Y	G	S	K	
<u>CCCATTGGGATCTATGGGTCGAAAAA</u>								
W	S	H	P	T	A	A	S	
<u>GTGGAGCCACCCCCACCGCTGCCCTCCA</u>								
cctctccagggtggctggccatgg								
tccttccccccacccttttttgag								

Fig.2(x)

SUBSTITUTE SHEET (RULE 26)

13/43

g3908	acagcgcttcaggtagcg
g3953	gtcaaggatgacctcgagc
g3998	gacaatggccagtggccat
g4043	agtctatttagcctgtcat
g4088	tgacctcttgcataagagaac
g4133	tatccttaggctctctagag
g4178	ttacagccagttatcacat
g4223	acctatagaccacagtgcc
g4268	tgctggcccacccctccaa
g4313	taatatttgcataatcctcct
g4358	ccaggcattaacccaagtt
g4403	gtgggagggcctaagatg
g4448	agcccatggatctgcactc
g4493	tgtctggcctcagttccc
g4538	cggtccaagacacttcatt
g4583	cccatcccccacccgcttc
g4628	tacactgaaactgaactct
g4673	atgatgaaataatggggaa
g4718	gaagaggggtcaaaaaccagc
g4763	gggcctctccagggtctgg
g4808	aggggctggagcctggag
g4853	ctgcgattcttgcacggga
g4898	gagactgaagaagccgggg
g4943	gctgtggggccgaagctt
g4988	agtttatattatggcgtga
g5033	ctggggatggctgcggct

Fig.2(xi)

SUBSTITUTE SHEET (RULE 26)

14/43

catgctggccttaaattcagtagtgc
tcctggtcttttgtctccacttaga
caccacctttgggagactagccatgg
ttggtgacagatggagtacaacagtg
tgaagacaggctgttttaaccccaa
gttaacttatataaaaatagagagacta
ggtcccacagaaccccttgcacaca
tgtgcctaccacataagggtctctac
cccttaaaaggtaaccttaggcagcct
acctcagcctttgaatgctcagaaa
tctcttctctgggtcccttcttaag
acttccttgcctgaagactctccg
tctaataatgaaatatattgcataaaa
cacctgtcaggttttaggcagcact
atggcaggcagttataagaagaagct
ctccgggtccctaagacagaataacttc
cgcagacgcataatgctcacttaatg
actgaggctccgagagattcctggag
tccaggaagctctccagccccatcc
gcttggcgggagtgaaacacagctggg
ctttggcccttgctcgtgcccgac
gccagcaggcggctgcgtccgcccga
gtagggttggaggaggaggtaaagcaggg
gtgccaggccctgtcagcgagtcccc
ggccgatgtccttatccgctggcctg
ggggattggacccaagggtggcttc

Fig.2(xii)

SUBSTITUTE SHEET (RULE 26)

g5078	ccactcagtcctccagccc
g5123	tgaggcttatcttggaaac
g5168	ctatttctgtcattcactt
g5213	aatataactacgtttaaa
g5258	ttcgtgagcgtgcgtgccat
g5303	tttgtgagtaggctcctt
g5348	caagagcaattactgagtc
g5393	tcccatcctgtttggatag
g5438	ggcttaattcgttagcta
g5483	gctaccacgttgtggag
g5528	gacacagtcccaagatctc
g5573	gcccttgcttgcgtgt
g5618	cattgactggtcttcctt
g5663	ctgatttgactccctcctt
g5708	ccattcctctgggtgactc
g5753	actttccccagccgaagct
g5798	gcgcgcgcctcctgctggc
g5843	E R P G tcttag <u>AGCGCCCGGGCC</u>
g5888	G G E P S S <u>GGCGGCGAGCCCAGCTCGG</u> F L G W L K
g5933	<u>TTCCTCGGCTGGCTCAAGA</u>
g5978	F R L Y D Q <u>TTCCGCCTGTACGACCACT</u>

Fig.2(xiii)

16/43

actccatgtcacacccgtgcattctc
 ccgccttgttctgtgctgtctgtct
 tcccagagccttttatgcttt
 aattgctttgtataatgtgtgtgcc
 caacacacacacgtgaaggtagagaac
 ccaccatgtgggacttagggctggcga
 atctcgccagccccctcaccctcact
 tcataggtaatcgaaggtaaatcgct
 tcctgcctcagcctaccaagtgctgt
 gggctctcctcccagtgtctgggggt
 tgctttctaggtctttgtcttagtt
 ccctagagtctccggccccacttac
 taccgaataactcggtttacacctcca
 tgcttgcctccatcgccgtggcattg
 tgggtccacacacctgacacaccttccca
 ggtctggatatgggaggccgcgtccc
 cgcgccccaacactgcccgtccattc

P G G G V C E P R
CGGGCGGCCGGGTGTGCGAGCCGCGG

G P V R R E L K Q
GCCCCGGTGC GGCGCGAGCTCAAGCAG
 K H A Y C S N L S
AGCACCGCATACTGCTCGAACCTTAGT

W R A W M Q K S H
GGCGTGCTTGGATGCAGAAGTCACAC

Fig.2(xiv)

SUBSTITUTE SHEET (RULE 26)

17/43

	K T R N Q V
g6023	<u>AAGACCCGAAACCAGGTAG</u>
	G K G A E E
g6068	<u>GGTAAAGGAGCAGAGGAAG</u>
	Q H R T L L
g6113	<u>CAACACCGCACCTTCTTT</u>
	P R A D G V
	P S G R R G A
g6158	<u>CCTCGGGCAGACGGGGTGC</u>
g6203	<u>GTGGGGCCTACAGCAGTCT</u>
g6248	<u>TGTTGCTCAAAGGGATCTC</u>
g6293	<u>GAGCCCCAGGTTTACTGC</u>
g6338	CTTAATGTGGCCTCTTTTC
g6383	* <u>CTAAGGATAGGCCATCCTC</u>
g6428	CTGAATTGGAGCCCCTCTG
g6473	CCAGAGGCTGGGCACAATG
g6518	ACATGATGGTCACACTTGG
g6563	GGTATTGCAGGGCCTCCCA
g6608	TTGTTCAGGTcccgtggc
g6653	gggggggg

Fig.2(xv)

18/43

G K L G E A C V G
GAAAGTTGGGGGAGGGCTTGCCTGGGG

E R D P G E Q P P
AGAGAGACCCGGGTGAGCAGCCTCCA

S K H R T R G S C
D E G I L
CCAAGCACAGGACGAGGGGATCCTGC

R R E V R G S G *
A R
GGCGAGAGGTAAGGGGGTCTGGGTGA
AGATGAGGCCCTTCCCCTCCTCGG
TTAGTGCTCATTCACCCACTGCAAA
ATCATCAAGTTGCTGAAGGGTCCAGG

V L P A K L
G P A G *
TGCCCTCAGGTCTGCCGGCTAAACT

CTGCTGGGTCAAGACCTGGAGGCTCAC
TACCATCTGGGCAACAAAGAACCTA
AGCTCCCACAACCACAGCTTGGTCC
ATATACCCCAGTGTGGTAGGGTTGG
AGAGTCTCTTAAATAAAATAAGGAG
cagtgtgtttggggccatatgtgctgg

Fig.2(xvi)

SUBSTITUTE SHEET (RULE 26)

19/43

20/43	21/43
22/43	23/43
24/43	25/43
26/43	27/43
28/43	29/43
30/43	31/43
32/43	33/43
34/43	35/43
36/43	37/43
38/43	39/43
40/43	41/43

Fig.3

SUBSTITUTE SHEET (RULE 26)

20/43

GCGGCCGCTG CAGTGATTAC TCACCGCGTG
TTTTTCCGTG GGGGGATGTG AAGAAAGTTA
GGAATGCAGG GTTCGGTCCC GTTCCCCAAA
AAGGGCTCCC TGCACGCGCT CCGGGACATC
TGAGAAAGGA CCAGAGGCCG GAGACTCCCT
ACGAAACGAG ACTACAGCGA TGGGAGAGGT
GACCCATGCA CCCAGAGAAA GGGACTGGTG
AGGGCTGAAA GAGGATGAAC GGGCTCAGGT
TGGGTATGGG GGCCCCGTAA GAGGGCGGG
GGAGGGGATC CTGGAAAAGC ACCAGGGCTG
ACAGGATCCC AGATGAGGGG GTGGGAAGCC
CACGGGCTGG TGGGGAAAGA GTGGGGGGCT
GTAACTGGC GGAGGCCGGC CGGGCGGGGC
GTGCGGGGCC CACGATCAAC CCCCCCCCCAG
CGGGGCGAGC GGCGCATTAG CGCCTTGTCA
CGCTGTCCGC GCCCAGTGAC GCGCGTGAGG
CGCCCCCGCC CCATACCGGC GTTGCAGTCA
GGGTCGCCCG GGCCCCGTG CCCAATCCGC

Fig.3(i)

SUBSTITUTE SHEET (RULE 26)

21/43

GCGCACCCCA	CCCGCGGGCC	GCTGAGTGGA	60
GGGAGAACTC	TTCTGCACCG	ATGGGAACTA	120
GGACACACACT	CTCCCCATAA	GCCCACTCAT	180
CCCATATCCA	ATACCCGCAG	ATATGATAGT	240
CCCTGCCTTC	TGGCTTCCC	CCCCCCCTGC	300
GGCATGAAGG	CTTAGGGTGG	GGATCGGTAG	360
GCAACTTTCA	AACTCTCTGG	GGAAGGAAGA	420
ACTGCTCAAT	GTGTGTGTGG	CGGACCAAAG	480
GAAGGTGGAT	AGGAAGGATC	CCGGTAGACT	540
CGAGCTAGGA	ACCCATTCTGG	AGTTAAGGGT	600
TGGGACGGGC	GGGACCAGAG	AGGGAGGTCC	660
TCGCGCAGGA	GGATGGGACG	TTCAGGAGTG	720
GCGCGGTGCC	CGCGGGCGGT	GGGAAGGCCG	780
GGGCCGGGCC	GGGCCGGGGG	CGGGGCCGGG	840
ATTCGGCTG	CTCAGACTTG	CTCCGGCCTT	900
ACCCGAGCCC	CAATCTGCAC	CCCGCAGACT	960
CCGCCCGTTG	CGCGCCACCC	CCATGCCCGC	1020
CGGGCGGCCG	CCGCGGCCGC	TGTCCCTCGCT	1080

Fig.3(ii)

22/43

GTGGTCGCCT CTGTTGCTCT GTGTCCTCGG
GTACCGTGCG CCCTGCTCCC CACCTCCCCA
AGTCGCGGGG GATGGAAGAA GGGGCGCGAG
GGCGGCCCTC GGGGCGCCCT CACCTGTGGG
AGTACCCCGT TATACATCAG AGGCCTCTTA
AGGCTCAGTT TGAAGGACAT CGCAGTGTCC
GCTTCGGGGC GCACGCCTGT GTCTTGGATA
GGGCGCACGC TTGGGTGCGT TGGGTTGGGT
GAAGTGATGA TCCCCGGGGG GAGGGTGGGG
ATGCGGCCCG GCGTCCCTCG GGACTTGCCT
CTATAGCAGA CTCCATGCTT TGGTATCCTC
CGGTCTCATT CAGGCTGCGC TGGGTTGAGA
CGAGAGCAAG CGTGTCCGGG CACCGCGAGC
GGGGGTCAAG TGCCGAGAGA ATCCCACTGT
ATCACCCAAAC GCACACATCC CCGCCAGGAT
CACACCCAAA GACACACAAA AGAGCCCCAC
CGCGCGCTGC AGCCCAGATG CGTATTGCA
ACACACACAC ACACACACAC ACACACACAC

Fig.3(iii)

SUBSTITUTE SHEET (RULE 26)

23/43

GGTGCCTCGG	GGCGGATCGG	GAGCCCGTGA	1140
GGGAAGCCGG	GATCCGGCGC	CCCGGGGGGT	1200
CGCCACCTGG	ACGTCCCAGG	AACAAAGGAA	1260
GCTCATGGCA	CCACCACCCA	GCCTCCCAAG	1320
TCTGTATCCC	CTTGCGAGG	CTGTCTGGCC	1380
TGGGACCCCC	CTCCTTCAGG	GTGCTGGGAC	1440
TCAGAGCGGA	AGGAAAGCCT	CCCTGGCCGG	1500
GCTGGCGCAA	AGTGGGGTCC	CCTCCCCCAT	1560
CGTTATCGTG	AGCCCTCCTG	TCCGCCTGGC	1620
CTCCGTGGGG	TCGGCGCCGC	CCCCTCCCCC	1680
GAAGTCCTCT	CCACTGGTGG	GGCTCACAAAC	1740
GCCTCTAGCG	ACTGAAATT	CGGTGAGGAG	1800
CCAGACTTCA	TTGTCTAAGG	GGCACCCAGT	1860
CCCAGGGAGGA	ACTCCTGGCC	TTGAGCCCCC	1920
GCGGTCTCCA	CATCCAGACC	CTCTCTGGGA	1980
TGGCTTATGT	CCCGTCACCC	TGCCCTCCGA	2040
CACCATCGCG	GCGCTCGCAT	TCCATCCTCT	2100
ACACACACAC	ACACACAGAC	ACGCACACAC	2160

Fig.3(iv)

SUBSTITUTE SHEET (RULE 26)

24/43

ACACGCACGC ACACACACGC ACGCCCGCAC
GCAACACCGG GGTACGCATA TGGTTGAGTG
ACCCCATCCG GAGACACAGG CCACACCGCA
TAGTAGTCTT GTGCAGTTG TCCGCGGTGT
ACAGGAAACCT ACACTCCTGC TTGCCCAAGG
GACCTTCGCG GGGAGTTGGT GTTGCTGCCA
GCGCTAACGCT TTGTTCCGG GCAGGGCTGCA
TGGCGCGTGT GTTTTTCTT TTAAGGGGGA
TGCAATCTGT TTGTACTTAC CGTGTGTCTT
AAAGTGTATG CAGGTACCAG CGGGACAGGA
GAGGCCACCT TCCCGTTGGC CTTTCAGGGA
GTGTTCTTT TAATAACGGC AGCAACTCCG
GGCCCCGGCT TTGTGGAAAG GAGGGGAAGA
GGCTTAGGGG GCTGTCAGCT GCTGCTCTGT
AGTGGCTTG GCCCATTGTT TGTGGAAAGCC
TACTCCAGAG TCAGGCTTCT CAGTCCGAGC
GAATCAGGGA AGGGGGTGCC AGGTGGACTA
AAGGAGAAAG CTTGGGCTTG CCCCCCTCCC

Fig.3(v)

SUBSTITUTE SHEET (RULE 26)

25/43

TCGTGGTCCC	ACATTTATTT	CACAGGGGAG	2220
CACTGGAGAT	CTTTCCCCAC	CACTCTCAGG	2280
GGGGCACCAAC	GCTGCGCTGC	TGCTCTGGGC	2340
CTGTGGACGC	CCTCCCGCTC	TTGTCAGGGG	2400
CGGCTGGGCA	GGTGATGTGG	TGACACCCGG	2460
AGCCTGGGTA	GTTTTGAAT	GCCACCAATA	2520
GAGCAACAGG	CGAAGGTGGC	GGAGTGGGGG	2580
GAGAAATTAA	ATAAGAGGTT	CTCACACCTC	2640
AACACCTGAC	CAGCCAGCCG	GTGGGTCGTA	2700
GATGGGGGCC	CCTGGGGTAT	GGCTGGGATG	2760
ATCTCACACT	TTTCCCTTTT	AAAACACATG	2820
CATTGGGAAA	GGGGGAAATA	AGCTTGTATA	2880
GGGAAGAAAA	AAGGAGGGGT	GTCTCCTCCA	2940
CTAGCTTGGC	ATGTGTGTGC	CCCAGTCCCC	3000
AAGAGGGAGA	CTGGAGTCCT	CTATCTCTGG	3060
CCAGAGAACG	TCTTCCCTGT	TTTATGGAGG	3120
CGTTCTGCTG	AGGACTGTAC	CAGTCGCTCG	3180
CCCTCAAGCC	ACGAAGGGCA	GCTGCTAGGC	3240

Fig.3(vi)

SUBSTITUTE SHEET (RULE 26)

26/43

TAGTGTGGTA AAAGGGCATT ACTCCCCAGC
CAGACAAATG CTGGGGAGGG ACAGAGGGGT
GGTCCCAGGT CGGGCAGTGC CTCCCACCCCT
GGGTGGGCCG GGGTAGAGAC GCTGGCACGT
GCGGGCGGCT GGCTGCCTGG GACCTCCGGG
GCCTGCTCCT CCTGCTCCTT CGCACGGACG
CCCAAATGCA ACTGCGATTG CAGGCTTCGC
CCTGGGAGAA GTCATTCAAGG GCCCAGACTA
GGGCATGAAG GACCGTCCAG GGCTGCAGTT
GCAGCCTCTG TTCTCCGAGC CTCTTGAA
AATACTCTT TCCTCTCATC CCATCCCAGG
TGCAGTCTTC CCTAACCTTT TCTTGCTTC
CCTCTCCCT TGCCCAACTG GGGCTCCAGC
CAGGGCCTCT CTGACACACA GGGTTGTAGC
CTCTTTGCT TCTGAGACTT AATTTTTTC
TCTCTGTACA GCCCTGGCTG CCCTGGCACT
ACAAACCTAC CTGCCTCTGC CTTTCCAGTG
AGTAGTTAAG TGTTTGCTG TGTCTTTATT

Fig.3(vii)

SUBSTITUTE SHEET (RULE 26)

27/43

CAGGACCCCC	CAGAGAGTCC	CCTTCCTGGC	3300
GTGATCATTG	CCCAGGGAGTG	CAGACAGTGG	3360
GCTGAGGGGG	GCGCCCAGGC	AGGAAGCGGT	3420
CCCAGTTCAT	GCCGAAGGAA	TTCTGAATT	3480
GC GGCCCCCT	GGCCCCCGCC	GCTCCGTCTG	3540
CTGAGACCTC	CGCTGAGCCC	TGGGACAAGC	3600
AAGACCCGCC	TCCTCCCAAG	GCCAAATTG	3660
GAACCATGTT	GGTGCCACCT	CATCCATCTG	3720
TAGCTTCTTA	ATAGGAACCT	GGGGGTGGGT	3780
ATCGGTTTG	TTTTGTTTT	TGTTTTTTCC	3840
ACTGTTTCC	TCCCTAAGGG	TTGAGAGCCC	3900
TACCCCAGGG	CCTTGACACA	TGGAGTCCA	3960
CTTACTGCAT	TTGGCTCTTG	GTAAGTGTCC	4020
CCCAGCTCCC	TCTCTTCTCC	TCCCCCCTTT	4080
TTTTTCTTT	TGGCTTTTG	AGACAGGGTT	4140
CATTCTGTAG	ACCAGGGCTAG	CCTCAAAC	4200
CTGGCACTAA	AGATGTGGGC	CACCACAACT	4260
CCTATAGTGA	CCTCAGTTCC	TGGCATATTG	4320

Fig.3(viii)

SUBSTITUTE SHEET (RULE 26)

28/43

TAGGCGATGG ATGGATGAAT GGATGGATGG
CTTGAATCGT CCTGAGTGAA AAAAGAGACC
GGCAGCCTGG CCTGCTGGTC TCATGGGAGC
CACCCCTGCCA TCCTGTGTGG CTGACAAGAA
AGGGAAAGCTT GGAATATGTT CCCCTCCTCA
CCAGCCTATG AGTAGGGCAG CTGTGGGCTG
GTCCCTCAGG GTGGGTCACA GGATTGAGGT
AGGAAATGAT TGTGGAGAGT CAGAACTCCT
GCTTCTGTGG CTGTCCCTTC TCTTGTGGTC
TGTGAGGAGG GCACGGGGAA AATGAAGGCT
CCAACAGGGC TCACCTCTCC TCTGGACAGG
TTTGATTCCC TTCCTTTGGT CTCCTGGGAT
TTTTAGATAT GTCCATTCTC CAGAAACACA
ACCACCAAGGA CAGACAAAGA ATTGGAGAGG
TGGCTTATGT GTAATCCCAG AACTCTGGAC
CAGTGTGTTG TAGGTAATGA GACCCTGTCA
ATGTTTATAG GCTGTGAGAC AGCTTGGTGG
CCTCAGCCCC ATCCCTAGGA ATCCATGGTA

Fig.3(ix)

SUBSTITUTE SHEET (RULE 26)

29/43

ATGGATGGAT	GGATGGTTGG	ATGGAGCAAG	4380
TCAGAGAACT	GAATGGAGTT	AGGTTCCCGAG	4440
TCCCTGTGAA	ACTTCCCCCA	CACCTCCCAC	4500
AGGCCAATGG	CCAGATGGGG	ACACAGACTC	4560
TATCCTAGGC	CTTGTGTTGTCC	CCCTGAGGGC	4620
CCCTAACGTT	GGGTAGGCAG	GAAGGGGGTG	4680
CATTTCCAAA	GTGGCCATCA	CAGTGGCCCT	4740
GTTGGGAGTT	GTAGAGGGCC	TTGCATGTGG	4800
CTTTGCACAG	TCCCCTCGTG	TGTGCTGGGA	4860
CAGCCCCCTGA	GCTTGCCCTT	CACGGTTTCAC	4920
CTCTCACTGT	ATGCACAGAT	TGGCCTCACA	4980
GACAAACATT	TACCAGGGTA	GGATTTTACA	5040
CTTGTGAGGT	TAGGGTATCA	GTGAAAGGAC	5100
AAGGAAATTG	GTAAGCCAGG	CCATGCTTGA	5160
GCTGAGGCAG	GAGGATTCCA	AGTTTCAAGA	5220
AGAAAAAGAAA	AGAAATAAAG	AGACAAGAAA	5280
GTAAGGGGCA	CTTGCCTCCA	ATCAAGATGA	5340
GAAGGAGAAA	GCAAACCTCA	GCTGCTGACC	5400

Fig.3(x)

SUBSTITUTE SHEET (RULE 26)

30/43

TCCATACATG TGCTCCAATG TGCACACACA
TTTGCTTAGA TTTGAGTAGG CATTATGAC
GAAAATATACT CTGTTTGTAT TTGGTTTGGT
GCTTCTCTGT GTAGTCCTGG CTGTCCTTGG
ACTCAGAAAT CCGCCTGCTT GTGCTTCCC
TCAGCAAAAT TGCATACTTT AACCCCAGTA
ATTCCAGGCT AGCCAAGGAT ACAGAGTGAG
CCAAAATGTA TTTTGTGCTT GTGTATGTAC
ACAACCTGTA GAAGTTCTCT CCGTTCACAG
AGGCTTAGCC ACAGTCTTCT TTATGTACTG
GAATTAATTT TTGAGATAAG GTCTCTTGT
AAGGTCACTCT TGAGCTGCTG GTACTCTTGC
GCAGCACTTC TCTGGGGAAG GGGCTGGCCT
GAGTGCTTGG GTCTCGTTGT TTCTTTCTT
GACTTCCTGA CTCTTGAAAC ATCCAGGCAG
GCCTAACAAA GTGTCGTCTT TGACCCCCAGA
CCTTCTCATC GGCTCCTCCC TGCAAGCTAC
CACCGCTGAG GGGCTCTACT GGACCTTCAA

Fig.3(xi)

SUBSTITUTE SHEET (RULE 26)

31/43

CAGGGAGACA	TAATCAATTAA	ATAGGATGTA	5460
TGATGTTTTA	AAATTTTAT	TTGATTTAT	5520
TTGGTTTGAG	TTTGTTTAT	TTGAGACAGG	5580
AACTCACTCT	GTAGACCAGG	CTGGCCTTGA	5640
AGTGCTTAGA	TTAAAGGTGT	GCACTGCCAT	5700
TTTGGGAGGC	AGAGGCAGAC	TAATGTGTGA	5760
ACCCTATTCT	TACCCTCCCC	CCCCAAAACC	5820
ATGTGTGTTG	CAGCACGTAA	ATGTCCAAGG	5880
TCTAACGT CCT	GAATTCAAAC	TAAGGTCCCTC	5940
AGCCATTTCA	CTGGCCCTGG	ATTGACTGAT	6000
GCTCTAGCTA	GGCTCAAAC	ATGAACTCCC	6060
TTCCACCCCA	AGTGGTGGAA	TGATACTCAG	6120
TGGCCTTGAT	TTTGTTCCT	CAGCTTCAAT	6180
TATCTGTGAA	ATGGGTGAAC	ACCTGTTCAA	6240
GGTGAGGGAC	TTGAAGTGGG	CTCATCCCAT	6300
CACAGCTGTA	ATCAGCCCCC	AGGACCCAC	6360
CTGCTCTATA	CATGGAGACA	CACCTGGGGC	6420
TGGTCGCCGC	CTGCCCTCTG	AGCTGTCCCG	6480

Fig.3(xii)

SUBSTITUTE SHEET (RULE 26)

32/43

CCTCCTTAAC ACCTCCACCC TGGCCCTGGC
GTCAGGAGAC AATCTGGTGT GTCACGCCCG
CTATGTTGGC TGTAAGTGGG GCCCCAGACA
GATTAGAGC CTGGGTCTTC TGTCCCTGGGG
CATGGTCATA CCCAGCACAG GCATTGCAAC
TGTGTACCCC ACAGCTTTAG AAAAGCTGTC
CCTTTAACAT CAGCTGCTGG TCCCGGAACA
GTGCACACGG GGAGACATTG TTACATACCA
TACCCAGCCA AGCCTTGCTG TGTGACTTCT
TTCCTGTTA TGAACCTAAA AGGGACTCTC
CACATGTGAG GAGTACCACA CTGTGGGCC
CCTCTTCACT CCCTATGAGA TCTGGGTGGA
TGATGTCCTC ACACTGGATG TCCTGGACGT
GCCCTAGACC TTATAGGGCG CCTCCCCCCC
GTCTTAGCCA CAGCCACGGT GGTTGCAGGA
TTTCCCCCAA GACAGTCAAG ATTTTCCCCT
CTCTGCAGAG AACACCTGGC CTGACCACCC
GAGTCCTAGG GGACTGAGAG GAGGCGCCCA

Fig.3(xiii)

33/43

CCTGGCTAAC	CTTAATGGGT	CCAGGCAGCA	6540
AGACGGCAGC	ATTCTGGCTG	GCTCCTGCCT	6600
CTCAGAGATA	GATGGGGGTT	GGCAATGACA	6660
CAGAGCCATG	GGCTCTCACT	TGCATGCAGG	6720
TCTAGGGACA	GCTGTGGCTG	CACTGTCCCC	6780
ATGTTTCCT	TGTAGTGCCC	CCTGAGAAGC	6840
TGAAGGATCT	CACGTGCCGC	TGGACACCGG	6900
ACTACTCCCT	CAAGTACAAG	CTGAGGTTGG	6960
GGCAATACTT	ACCTTCTCTG	ATCAAATATG	7020
GCACCTCCAC	AGGTGGTACG	GTCAGGATAAA	7080
TCACTCATGC	CATATCCCCA	AGGACCTGGC	7140
AGCCACCAAT	CGCCTAGGCT	CAGCAAGATC	7200
GGGTGAGCCC	CCAGTGTCCA	CCTGTGTTCT	7260
ATCCCCCCCAG	ACTTTTTGGT	TCTTCTAGAG	7320
CAGTGGTTGT	TCATAACTTA	ATGCAAAGAC	7380
CCCCACCCCC	AACACACACA	TACACACACA	7440
TCCCTCTCTA	CAGCCCAGGT	GTTCAGAAGG	7500
GGTCTGAAGG	CGCCCCAGGA	AGCCGAGGCC	7560

Fig.3(xiv)

SUBSTITUTE SHEET (RULE 26)

34/43

TTGAGCTGGG GGGGGGGCG AGGGTTGGAG
GGGCCTAACATC TAATTAGGGT GTTCCCAGCC
GTGCCTCACT GAAGACTCAG GGGAGAGATC
GGGTTCCCTGG GTGCCCTGG CTCATTCCA
TAACCCCTCAG TTGTGCTCTG TGGCTGGCAC
CAAGGCATCA GAGGTGGACA TGGGATGGGG
AAGGTGGGGT GATATAACAAT AAAGCTTGTC
GATCACAAATT GTTGACATCA CTCTGGGACA
AGTAGCTTTA AGAGTCAGCT TGTGACTTAA
GTGATGCTCG CCTCACTCCC TGTTAGTGA
GTGGGCTGCT CTGTCCCCCTT GAGGGCAGGA
TGGTAGCAGC AACTGCTGCT GGCTGTTCT
CTGGGTGAGT AGCTAACAGG GGTGGGGCG
AGCCACTGCA GCCTAGATTA CACCACTGGG
AGTCCTCAGA ACTGGGAGCA CTGTTGCCAG
AGGGGAGGCA GAGGCAGAAG GATCTCTCTG
AGCTCCAGGC CAGCCAGGGT GCGCAGTAAA
TGACCAGGCT TGCTCCACCC CCAGTGACCA

Fig.3(xv)

35/43

GCACGAACTG	GATGATCCCT	GAGCACAACT	7620
CAAAGCAGCC	TGGGCCATT	AACCCTTCAA	7680
AGCTTGTACT	CTCTCCATGG	TCCCCCAGGA	7740
CATCCAGAGG	TTTTGTGTCT	TCCTGGCATC	7800
AGCTGCCCG	TGGAGGCTCT	TGGTAATGTA	7860
ATACATAGGG	ATGGAGCCAA	ATAGCACCTC	7920
ACCCTGACGC	TCAGAAAGCC	TACTCATGAT	7980
TGTAGTGAGA	CCCTAGCTCA	AAACACAGAC	8040
TACTGGAACT	CAGGGCCTAA	TAGGTGCTGG	8100
GATCTCTGCG	CTAATCTCCA	CCCCAGCTGG	8160
ATGTGTGTCT	TCCATCAGAG	ATAGGACCCG	8220
GGAATATTAA	ATGACAGTAA	TCTATCAGGC	8280
TGGTCTGGAA	AACGCAGATA	GGGTCATAGG	8340
TGTTCTGTCA	CTAGGCCATT	CTCACCAAGC	8400
CATTTAATGC	CAGCATTAA	TGCCAGCATT	8460
AGTTCAAGGC	CATCCTGAAT	TTACATAAAG	8520
ACCTTGTCTC	AAAAAACAAA	GCATCTTAG	8580
CGGACCCCCC	ACCCGACGTG	CACGTGAGCC	8640

Fig.3(xvi)

36/43

GC GTTGGGGG CCTGGAGGAC CAGCTGAGTG
ATTT CCTCTT CCAAGCCAAG TACCAGATCC
AGGTGCCCGT CCCGCCCGG ACCCGCCCCT
CACCGTGCAG GTGGTGGATG ACGTCAGCAA
GCCCGGCACC GTTTACTTCG TCCAAGTGCG
AAAGGCGGGA ATCTGGAGCG AGTGGAGCCA
TGAGCACCTC TCCAGGGCTG GCTGGCCCAT
CCCACCCCTT TTTTGAGACA GCGTCTTCAG
TAGTCAAGGA TGACCTCGAG CTCCTGGTCT
GGCCATCACC ACCTTGGA GACTAGCCAT
GATGGAGTAC AACAGTGTGA CCTCTTGTAA
AATATCCTAG GCTCTCTAGA GGTTAACTTT
TCACATGGTC CCACAGAACCC TTTTGTCA
CACATAAGGG TCTCTACTGC TGGCCCACCC
CTTAATATTG GCAATCCTCC TACCTCAGCC
CAAGTTCTC TTCTCTGGGT CCCTTTCTTA
GTCCTGAAGA CTCTCCGAGC CCATGGATCT
AATGTCTGGC CTCAGTTCC CCACCTGTCA

Fig.3(xvii)

37/43

TGCGCTGGGT	CTCACCAACCA	GCTCTCAAGG	8700
GCTACCGCGT	GGAGGACAGC	GTGGACTGGA	8760
GACCCCGCCC	CCCGCATCTG	ACTCCTCCCT	8820
CCAGACCTCC	TGCCGTCTCG	CGGGCCTGAA	8880
TTGTAACCCA	TTCGGGATCT	ATGGGTCGAA	8940
CCCCACCGCT	GCCTCCACCC	CTCGAAGTGG	9000
GGAATCCCCA	ATCCATCCTG	TTCCCTTCCCC	9060
GTAGCGCATG	CTGGCCTTAA	ATTCAAGTATG	9120
TTTTGTCTCC	ACTTAGAGAC	AATGGCCAGT	9180
GGAGTCTATT	TAGCCTGTCA	TTTGGTGACA	9240
GAGAACTGAA	GACAGGCTGT	TTTTAACCCC	9300
ATATAAAATA	GAGACTATTA	CAGCCAGTTA	9360
CAACCTATAG	ACCACAGTGC	CTGTGCCTAC	9420
CTCCAACCCT	TAAAAGGTAA	CCTAGGCAGC	9480
TCTTGAATGC	TCAGAAACCA	GGCATTAACC	9540
AGGTGGGAGG	GCCTAAAGAT	GACTTCCTTT	9600
GCACTCTCTA	ATATGAAATA	TATTGCATAA	9660
GGTTTAGGCA	GCACAGTCGG	TCCAAGACAC	9720

Fig.3(xviii)

SUBSTITUTE SHEET (RULE 26)

38/43

TTCAATTATTT GCAGGCAGTA TAAGAAGAAG
CTAAGACAGA ATACTTCTAC ACTGAAACTG
TGATGATGAA ATAATGGGGA AACTGAGGCT
ACCAGCTCCA GGAAGCTCTC CAGCCCCAT
GAGTGAACAC AGCTGGGAGG GGCTGGAGCC
ACCTGCGATT CTTGCACGGG AGCCAGCAGG
CCGGGGGTAG GGTTGGAGGG AGGTAAGCAG
CCTGTCAGCG AGTCCCCAGT TTTATTTATG
TGCTGGGGGA TGGCTGCGGC TGGGGATTGG
CAGCCCACTC CATGTCACAC CCGTGCATTC
TTCTGTGCTG TCTGTCTCTA TTTCTGTCAT
TTAATATAAC TACGTTTAA AAATTGCTTT
GTGCCACAAC ACACACGTGA AGGTTAGAGA
GGGACTAGGG CTGGCGACAA GAGCAATTAC
CTTCCCACATCC TGTTTGGATA GTCATAGGTA
TAGCTATCCT GCCTCAGCCT ACCAAGTGCT
TCCCAGTGTG TGCGGGTACA CAGTCCCAAG
TGCCCCCTTGC TTTGTCCGTG TCCCTAGAGT

Fig.3(xix)

SUBSTITUTE SHEET (RULE 26)

39/43

CTCCCATCCC	CCACCCGCTT	CCTCCGGTCC	9780
AACTCTCGCA	GACGCATATG	CTCACTTTAA	9840
CCGAGAGATT	CCTGGAGGAA	GAGGGTCAAA	9900
CCGGGCCTCT	CCAGGTTCTG	GGCTTGGCGG	9960
TGGGAGCTTT	GGCCCTTGCT	CGTGCCCAGC	10020
CGGCTGCGTC	CGCCCGAGAG	ACTGAAGAAG	10080
GGGCTGTGGG	GGCCGAAGCT	TGTGCCAGGG	10140
GCGTGAGGCC	GATGTCCTTA	TCCGCTGGCC	10200
ACCCAAGGGC	TGGCTTCCCA	CTCAGTCCTC	10260
TCTGAGGCTT	ATCTTGGGAA	CCCGCCCTTG	10320
TCACCTTCCC	AGAGCCTTTT	TTTTATGCTT	10380
TGTATAATGT	GTGTGCCTTC	GTGAGCGTGC	10440
ACTTTGTTGA	GTAGGCTCCT	TCCACCATGT	10500
TGAGTCATCT	CGCCAGCCCC	TCACCCCTCA	10560
ATCGAAGGTA	AATCGCTGGC	TTTAATTCG	10620
GTGCTACCAC	GTTTGTGGGA	GGGGCTCTCC	10680
ATCTCTGCTT	TCTAGGTCTT	TGTCTTAGTT	10740
CTCCGGCCCC	ACTTAGTCTC	CATTGATTTC	10800

Fig.3(xx)

SUBSTITUTE SHEET (RULE 26)

40/43

CTTTCTGACC GAATACTCGG TTTTACCTCC
CCATCGCCGT GGCATTGCCA TTCCTCTGGG
CAACTTCCC CAGCCGAAGC TGGTCTGGTA
GCTGGCCGCG CCCCAACACT GCCGCTCCAT
GGGTGTGCGA GCCGCGGGGC GGCGAGCCC
AGTTCCTCGG CTGGCTCAAG AAGCACGCAT
ACCAGTGGCG TGCTTGGATG CAGAAAGTCAC
GGGAGGGCTTG CGTGGGGGGT AAAGGAGCAG
CACAAACACCG CACTCTTCTT TCCAAGCACA
GGGTGCGGCG AGAGGTAAGG GGGTCTGGGT
CCTTTCCCCT CCTTCGGTGT TGCTCAAAGG
AAGAGCCCCA GGTTTTACTG CATCATCAAG
CTTTTCTGCC CTCAGGTCTT GCCGGCTAAA
CAGACCTGGA GGCTCACCTG AATTGGAGCC
TACCAGAGGC TGGGCACAAT GAGCTCCCAC
ACTTGGATAT ACCCCAGTGT GGGTAGGGTT
TTAAATAAAAT AAAGGAGTTG TTCAGGTCCC
GGGGTGGGGGG GA

Fig.3(XXI)

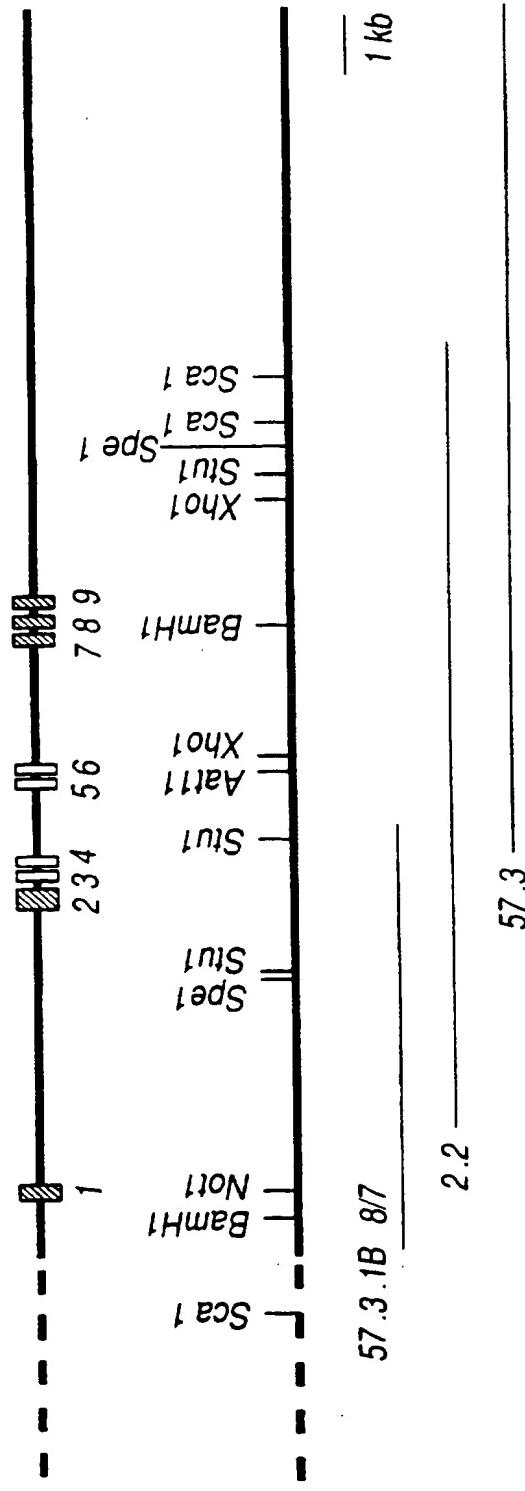
41/43

CACTGATTTG	ACTCCCTCCT	TTGCTTGTCT	10860
TGACTCTGGG	TCCACACACTG	ACACCTTC	10920
TGGGAGGCCG	CCGTCCCCGCG	CGCGCCTC	10980
TCTCTTTAGA	GCGCCCGGGC	CCGGGC	11040
GCTCGGGCCC	GGTGCGGC	GAGCTCAAGC	11100
ACTGCTCGAA	CCTTAGTTTC	CGCCTGTACG	11160
ACAAGACCCG	AAACCAGGTA	GGAAAGTTGG	11220
AGGAAGAGAG	AGACCCGGGT	GAGCAGCCTC	11280
GGACGAGGGG	ATCCTGCCCT	CGGGCAGACG	11340
GAGTGGGGCC	TACAGCAGTC	TAGATGAGGC	11400
GATCTCTTAG	TGCTCATTTC	ACCCACTGCA	11460
TTGCTGAAGG	GTCCAGGCTT	AATGTGGCCT	11520
CTCTAAGGAT	AGGCCATCCT	CCTGCTGGGT	11580
CCTCTGTACC	ATCTGGGCAA	CAAAGAAACC	11640
AACCACAGCT	TTGGTCCACA	TGATGGTCAC	11700
GGGGTATTGC	AGGGCCTCCC	AAGAGTCTCT	11760
GATGCCAGT	GTGTTGGGG	CCTATGTGCT	11820
			11832

Fig.3(xxii)

42/43

MURINE NR-6 GENOMIC STRUCTURE



LIBRARY: MOUSE 129/Sv FEMALE LIVER

MURINE NR-6 PROTEIN

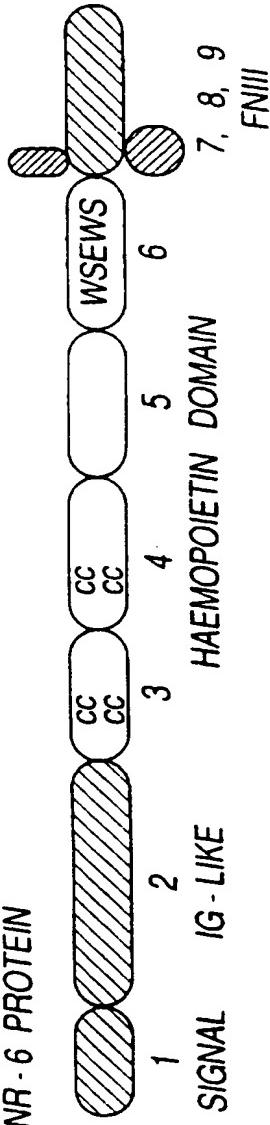
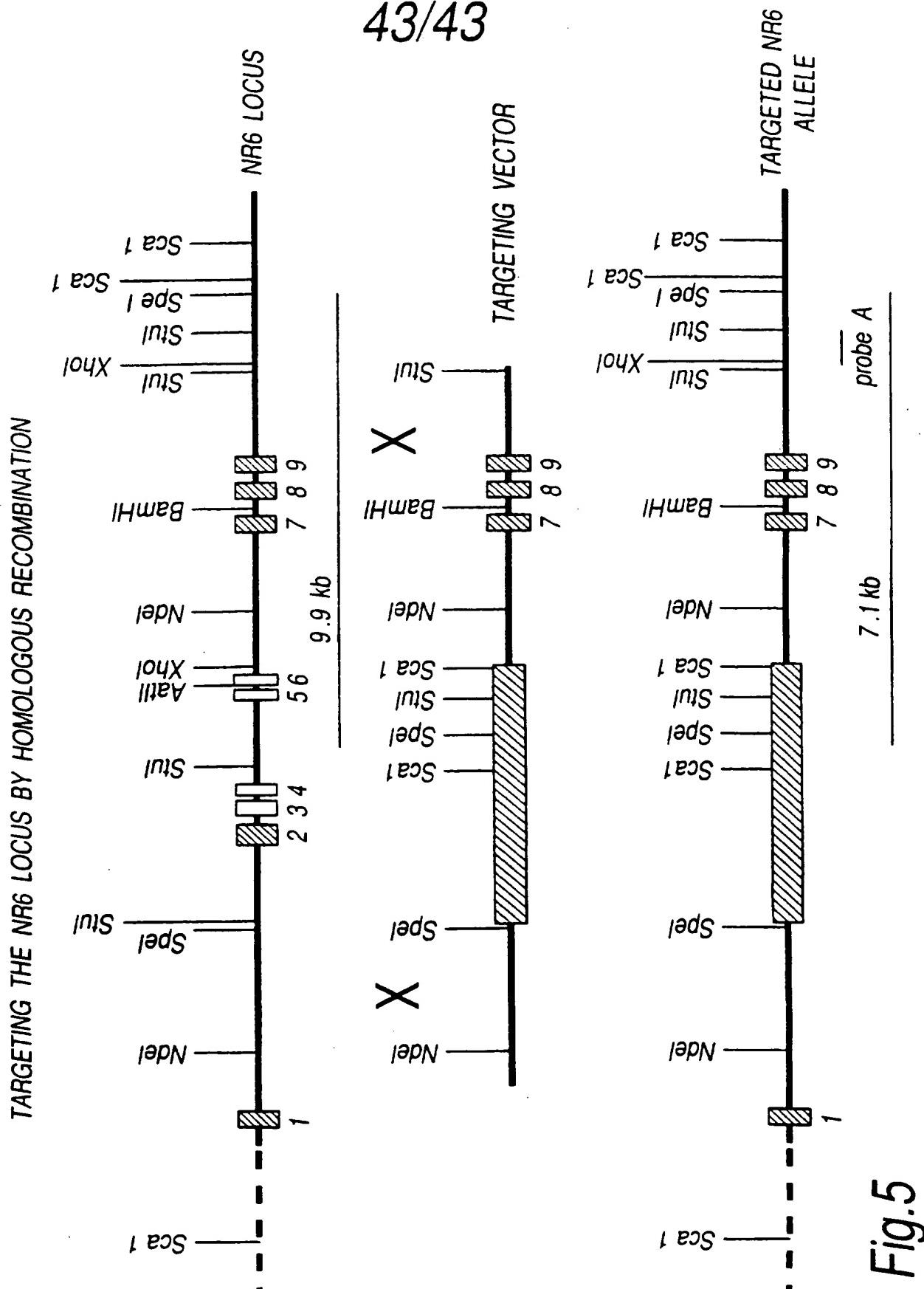


Fig. 4

43/43



SUBSTITUTE SHEET (RULE 26)

THIS PAGE BLANK (USPTO)



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/19, C07K 14/715, A61K 38/17, C07K 16/18, A01K 67/027		A3	(11) International Publication Number: WO 98/11225 (43) International Publication Date: 19 March 1998 (19.03.98)
(21) International Application Number: PCT/GB97/02479		Kasuga, Tsukuba, Ibaraki 305 (JP). KIKUCHI, Yasufumi [JP/JP]; 1-29-5-110 Komatsu, Tsuchiura, Ibaraki 300 (JP). NASH, Andrew [AU/AU]; 24 Green Street, Northcote, VIC 3070 (AU).	
(22) International Filing Date: 11 September 1997 (11.09.97)		(74) Agents: DZIEGLEWSKA, Hanna, Eva et al.; Frank B. Dehn & Co., 179 Queen Victoria Street, London EC4V 4EL (GB).	
(30) Priority Data: PO 2246 11 September 1996 (11.09.96) AU		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(71) Applicant (<i>for all designated States except US</i>): AMRAD OPERATIONS PTY, LTD. [AU/AU]; 576 Swan Street, Richmond, VIC 3121 (AU).		Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(71) Applicant (<i>for GB only</i>): DZIEGLEWSKA, Hanna, Eva [GB/GB]; Frank B. Dehn & Co., 179 Queen Victoria Street, London EC4V 4EL (GB).		(88) Date of publication of the international search report: 30 April 1998 (30.04.98)	
(72) Inventors; and			
(75) Inventors/Applicants (<i>for US only</i>): HILTON, Douglas, James [AU/AU]; 244 Research Road, Warrandyte, VIC 3113 (AU). NICOLA, Nicos, Antony [AU/AU]; 56 Churchill Avenue, Mont Albert, VIC 3127 (AU). FARLEY, Alison [AU/AU]; 27/9-19 Miller Street, North Fitzroy, VIC 3068 (AU). WILLSON, Tracy [AU/AU]; 26 Fortuna Avenue, North Balwyn, VIC 3104 (AU). ZHANG, Jian-Guo [CN/AU]; 3 Karri Crescent, Hoppers Crossing, VIC 3029 (AU). ALEXANDER, Warren [AU/AU]; 13 Park Street, Moonee Ponds, VIC 3039 (AU). RAKAR, Steven [AU/AU]; 26 Riverside Avenue, Avondale Heights, VIC 3034 (AU). FABRI, Louis [AU/AU]; 8 Laver Court, Mill Park, VIC 3082 (AU). KOJIMA, Tetsuo [JP/JP]; 1-8-1-302 Minami-Rokugou, Ota-ku, Tokyo 144 (JP). MAEDA, Masatsugu [JP/JP]; 1-6-2-606			

(54) Title: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME

(57) Abstract

The present invention relates generally to a novel haemopoietin receptor or derivatives thereof and to genetic sequences encoding same. Interaction between the novel receptor of the present invention and a cytokine ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The novel receptor and its derivatives and the genetic sequences encoding same of the present invention are useful in the development of a wide range of agonists, antagonists, therapeutics and diagnostic reagents based on ligand interaction with its receptor.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

INTERNATIONAL SEARCH REPORT

International Application No
PCT/GB 97/02479

A. CLASSIFICATION OF SUBJECT MATTER
 IPC 6 C12N15/19 C07K14/715 A61K38/17 C07K16/18 A01K67/027

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMEST12 emb1 SEQ ID MM77631 Acc.No:W66776, 15 June 1996 "Mus musculus cDNA me17b11.r1 similar to PIR:B38252 granulocyte colony-stimulating factor receptor precursor" XP002055540 cited in the application & MARRA ET AL.: "The WahU-HHMI mouse EST project" .. ---</p>	1-10, 14-19 - / --

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

& document member of the same patent family

1

Date of the actual completion of the international search Date of mailing of the international search report

12 February 1998

06.03.98

Name and mailing address of the ISA
 European Patent Office, P.B. 5818 Patenttaan 2
 NL - 2280 HV Rijswijk
 Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
 Fax: (+31-70) 340-3016

Authorized officer

Cupido, M

INTERNATIONAL SEARCH REPORT

International Application No.
PCT/GB 97/02479

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ROBB ET AL.: "Structural analysis of the gene encoding the murine Interleukin-11 receptor alpha-chain and a related locus" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 271, no. 23, 7 June 1996, MD US, pages 13754-13761, XP002055539 see figure 3 ---	1-3,20, 21
X	WO 96 08510 A (PROGENITOR, INC.) 21 March 1996 see figure 2c nucleotides 1053-1068 on sheet 4/11 ---	1-3,20, 21
X	WO 96 07737 A (AMRAD OPERATIONS PTY.LTD.) 14 March 1996 see figure 8 nucleotides 1040-1055 on sheet 14/21 see claims 1,13 ---	1,3,13, 20
P,X	WO 97 15663 A (AMRAD OPERATIONS PTY. LTD.) 1 May 1997 see figure 7 (vii) on sheet 20/24 ---	1-3,20, 21
P,X	WO 97 12037 A (AMRAD OPERATIONS PTY. LTD.) 3 April 1997 see claims 1-3 ---	1-3,20, 21
P,X	WO 97 25425 A (GENENTECH, INC.) 17 July 1997 see figure 2b on sheet 12/85 -----	1-3,20, 21

INTERNATIONAL SEARCH REPORT

International application No.
PCT/GB 97/02479

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
see FURTHER INFORMATION sheet PCT/ISA/210
2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
- No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/GB 97/02479

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Remark : Although claims 28 and 29 are directed to a method of treatment of the human/animal body , the search has been carried out and based on the alleged effects of the composition.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/GB 97/02479

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO 9608510 A	21-03-96	US 5643748 A		01-07-97
		AU 3419495 A		29-03-96
		CA 2176463 A		21-03-96
		EP 0730606 A		11-09-96
-----	-----	-----	-----	-----
WO 9607737 A	14-03-96	AU 3465295 A		27-03-96
		CA 2197873 A		14-03-96
		EP 0804576 A		05-11-97
-----	-----	-----	-----	-----
WO 9715663 A	01-05-97	AU 7266896 A		15-05-97
-----	-----	-----	-----	-----
WO 9712037 A	03-04-97	AU 6980596 A		17-04-97
-----	-----	-----	-----	-----
WO 9725425 A	17-07-97	AU 1574797 A		01-08-97
-----	-----	-----	-----	-----

THIS PAGE BLANK (USPTO)

**CORRECTED
VERSION***

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : C12N 15/19, C07K 14/715, A61K 38/17, C07K 16/18, A01K 67/027		A3	(11) International Publication Number: WO 98/11225 (43) International Publication Date: 19 March 1998 (19.03.98)		
(21) International Application Number: PCT/GB97/02479		Kasuga, Tsukuba, Ibaraki 305 (JP). KIKUCHI, Yasufumi [JP/JP]; 1-29-5-110 Komatsu, Tsuchiura, Ibaraki 300 (JP). NASH, Andrew [AU/AU]; 24 Green Street, Northcote, VIC 3070 (AU).			
(22) International Filing Date: 11 September 1997 (11.09.97)		(74) Agents: DZIEGLEWSKA, Hanna, Eva et al.; Frank B. Dehn & Co., 179 Queen Victoria Street, London EC4V 4EL (GB).			
(30) Priority Data: PO 2246 11 September 1996 (11.09.96) AU		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).			
(71) Applicant (for all designated States except US): AMRAD OPERATIONS PTY. LTD. [AU/AU]; 576 Swan Street, Richmond, VIC 3121 (AU).		Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>			
(71) Applicant (for GB only): DZIEGLEWSKA, Hanna, Eva [GB/GB]; Frank B. Dehn & Co., 179 Queen Victoria Street, London EC4V 4EL (GB).		(88) Date of publication of the international search report: 30 April 1998 (30.04.98)			
(72) Inventors; and					
(75) Inventors/Applicants (for US only): HILTON, Douglas, James [AU/AU]; 244 Research Road, Warrandyte, VIC 3113 (AU). NICOLA, Nicos, Antony [AU/AU]; 56 Churchill Avenue, Mont Albert, VIC 3127 (AU). FARLEY, Alison [AU/AU]; 27/9-19 Miller Street, North Fitzroy, VIC 3068 (AU). WILLSON, Tracy [AU/AU]; 26 Fortuna Avenue, North Balwyn, VIC 3104 (AU). ZHANG, Jian-Guo [CN/AU]; 3 Karri Crescent, Hoppers Crossing, VIC 3029 (AU). ALEXANDER, Warren [AU/AU]; 13 Park Street, Moonee Ponds, VIC 3039 (AU). RAKAR, Steven [AU/AU]; 26 Riverside Avenue, Avondale Heights, VIC 3034 (AU). FABRI, Louis [AU/AU]; 8 Laver Court, Mill Park, VIC 3082 (AU). KOJIMA, Tetsuo [JP/JP]; 1-8-1-302 Minami-Rokugou, Ota-ku, Tokyo 144 (JP). MAEDA, Masatsugu [JP/JP]; 1-6-2-606					
(54) Title: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME					
(57) Abstract					
The present invention relates generally to a novel haemopoietin receptor or derivatives thereof and to genetic sequences encoding same. Interaction between the novel receptor of the present invention and a cytokine ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The novel receptor and its derivatives and the genetic sequences encoding same of the present invention are useful in the development of a wide range of agonists, antagonists, therapeutics and diagnostic reagents based on ligand interaction with its receptor.					

*(Referred to in PCT Gazette No. 26/1998, Section II)

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC
SEQUENCES ENCODING SAME

The present invention relates generally to a novel
5 haemopoietin receptor or derivatives thereof and to
genetic sequences encoding same. Interaction between
the novel receptor of the present invention and a ligand
facilitates proliferation, differentiation and survival
10 of a wide variety of cells. The novel receptor and its
derivatives and the genetic sequences encoding same of
the present invention are useful in the development of a
wide range of agonists, antagonists, therapeutics and
diagnostic reagents based on ligand interaction with its
receptor.

15 Bibliographic details of the publications numerically
referred to in this specification are collected at the
end of the description. Sequence Identity Numbers (SEQ
ID NOS.) for the nucleotide and amino acid sequences
20 referred to in the specification are defined following
the bibliography.

Throughout this specification and the claims which
follow, unless the context requires otherwise, the word
25 "comprise", or variations such as "comprises" or
"comprising", will be understood to imply the inclusion
of a stated integer or group of integers but not the
exclusion of any other integer or group of integers.

30 The rapidly increasing sophistication of recombinant DNA
techniques is greatly facilitating research into the
medical and allied health fields. Cytokine research is
of particular importance, especially as these molecules
regulate the proliferation, differentiation and function
35 of a wide variety of cells. Administration of
recombinant cytokines or regulating cytokine function
and/or synthesis is becoming increasingly the focus of

medical research into the treatment of a range of disease conditions.

Despite the discovery of a range of cytokines and other secreted regulators of cell function, comparatively few cytokines are directly used or targeted in therapeutic regimens. One reason for this is the pleiotropic nature of many cytokines. For example, interleukin (IL)-11 is a functionally pleiotropic molecule (1,2), initially characterized by its ability to stimulate proliferation of the IL-6-dependent plasmacytoma cell line, T11 65 (3). Other biological actions of IL-11 include induction of multipotential haemopoietin progenitor cell proliferation (4,5,6), enhancement of megakaryocyte and platelet formation (7,8,9,10), stimulation of acute phase protein synthesis (11) and inhibition of adipocyte lipoprotein lipase activity (12, 13).

Other important cytokines in the IL-11 group include IL-6, leukaemia inhibitory factor (LIF), oncostatin M (OSM) and CNTF. All these cytokines exhibit pleiotropic properties with significant activities in proliferation, differentiation and survival of cells. Members of the haemopoietin receptor family are defined by the presence of a conserved amino acid domain in their extracellular region. However, despite the low level of amino acid sequence conservation between other haemopoietin receptor domains of different receptors, they are all predicted to assume a similar tertiary structure, centred around two fibronectin-type III repeats (18,19).

The size of the haemopoietin receptor family has now become extensive and includes the cell surface receptors for many cytokines including interleukin-2 (IL-2), IL-3, IL-4, IL-5, IL-6, IL-7, IL-9, IL-11, IL-12, IL-13, IL-15, granulocyte colony stimulating factor (G-CSF), granulocyte-macrophage-CSF (GM-CSF), erythropoietin,

thrombopoietin, leptin, leukaemia inhibitory factor, oncostatin-M, ciliary neurotrophic factor, cardiotrophin, growth hormone and prolactin. Although most of the members of the haemopoietin receptor family act as classic cell surface receptors, binding their cognate ligand at the cell surface and initiating intracellular signal transduction, some receptors are also produced in naturally occurring soluble forms. These soluble receptors can either act as cytokine antagonists, by binding to cytokines and inhibiting productive interactions with cell surface receptors (eg LIF binding protein; (20) or as agonists, binding to cytokine and potentiating interaction with cell surface receptor components (eg soluble interleukin-6 receptor α-chain; (21)). Still other members of the family appear to be produced only as secreted proteins, with no evidence of a cell surface form. In this regard, the IL-12 p40 subunit is a useful example. The cytokine IL-12 is secreted as a heterodimer composed of a p35 subunit which shows similarity to cytokines such as IL-6 (22) and a p40 subunit which shares similarity with the IL-6 receptor α-chain (23). In this case the soluble receptor acts as part of the cytokine itself and essential to formation of an active protein. In addition to acting as cytokines (eg IL-12p40), cytokine agonists (eg IL-6 receptor α-chain) or cytokine antagonists (LIF binding protein), members of the haemopoietin receptor have been useful in the discovery of small molecule cytokine mimetics. For example, the discovery of peptide mimetics of two commercially valuable cytokines, erythropoietin and thrombopoietin, centred on the selection of peptides capable of binding to soluble versions of the erythropoietin and thrombopoietin receptors (24,25). Due to the importance and multifactorial nature of these cytokines, there is a need to identify receptors, including both cell bound and soluble, for pleiotropic cytokines. Identification

of such receptors permits the identification of pleiotropic cytokines and the development of a range of therapeutic and diagnostic agents.

5 Accordingly, one aspect of the present invention relates to a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a novel haemopoietin receptor or a derivative thereof.

10 More particularly, the present invention provides a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a novel haemopoietin receptor or a derivative thereof having the motif:

15 Trp Ser Xaa Trp Ser [SEQ ID NO:1],
wherein Xaa is any amino acid and is preferably Asp or Glu.

20 Even more particularly, the present invention is directed to a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a novel haemopoietin receptor or a derivative thereof, said receptor comprising the motif:

25 Trp Ser Xaa Trp Ser [SEQ ID NO:1]

wherein Xaa is any amino acid and is preferably Asp or Glu, said nucleic acid molecule is identifiable by hybridisation to said molecule under low stringency conditions at 42°C with

30 5N (A/G) CTCCA(A/G) TC(A/G) CTCCA 3N [SEQ ID NO:7]

and

35 5N (A/G) CTCCA(C/T) TC(A/G) CTCCA 3N [SEQ ID NO:8].

Still more particularly, the present invention provides an isolated nucleic acid molecule comprising a sequence

of nucleotides substantially as set forth in SEQ ID NO:12 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:12 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

In a related embodiment, the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:14 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:14 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

In another related embodiment, the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:16 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:16 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

In a further related embodiment, the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:18 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:18 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

In yet a further related embodiment, the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:24 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:24 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

Still yet a further embodiment of the present invention is directed to a sequence of nucleotides substantially as set forth in SEQ ID NO:28 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:28 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

In still yet another embodiment, the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides substantially set forth in SEQ ID NO:38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:38 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

The term "receptor" is used in its broadest sense and includes any molecule capable of binding, associating or otherwise interacting with a ligand. Generally, the interaction will have a signalling effect although the present invention is not necessarily so limited. For example, the "receptor" may be in soluble form, often

referred to as a cytokine binding protein. A receptor may be deemed a receptor notwithstanding that its ligand or ligands has or have not been identified.

5 Preferably, the novel receptor is derived from a mammal or a species of bird. Particularly, preferred mammals include humans, primates, laboratory test animals (e.g. mice, rats, rabbits, guinea pigs), livestock animals (e.g. sheep, horses, pigs, cows), companion animals
10 (e.g. dogs, cats) or captive wild animals (e.g. deer, foxes, kangaroos). Although the present invention is exemplified with respect to mice, the scope of the subject invention extends to all animals and in particular humans.

15 The present invention is predicated in part on an ability to identify members of the haemopoietin receptor family with limited sequence similarity. Based on this approach, a genetic sequence has been identified in accordance with the present invention which encodes a novel receptor. The expressed genetic sequence is referred to herein as "NR6". Different forms of NR6 are referred to as, for example, NR6.1, NR6.2 and NR6.3. The nucleotide and corresponding amino acid sequences 20 for these molecules are represented in SEQ ID NOS:12, 14 and 16, respectively.

25 Preferred human and murine nucleic acid sequences for NR6 or its derivatives include sequences from brain, liver, kidney, neonatal, embryonic, cancer or tumour-derived tissues.

30 Reference herein to a low stringency at 42EC includes and encompasses from at least about 1% v/v to at least about 15% v/v formamide and from at least about 1M to at least about 2M salt for hybridisation, and at least about 1M to at least about 2M salt for washing

conditions. Alternative stringency conditions may be applied where necessary, such as medium stringency, which includes and encompasses from at least about 16% v/v to at least about 30% v/v formamide and from at least about 0.5M to at least about 0.9M salt for hybridisation, and at least about 0.5M to at least about 0.9M salt for washing conditions, or high stringency, which includes and encompasses from at least about 31% v/v to at least about 50% v/v formamide and from at least about 0.01M to at least about 0.15M salt for hybridisation, and at least about 0.01M to at least about 0.15M salt for washing conditions.

The nucleic acid molecules contemplated by the present invention are generally in isolated form and are preferably cDNA or genomic DNA molecules. In a particularly preferred embodiment, the nucleic acid molecules are in vectors and most preferably expression vectors to enable expression in a suitable host cell. Particularly useful host cells include prokaryotic cells, mammalian cells, yeast cells and insect cells. The cells may also be in the form of a cell line.

Accordingly, another aspect of the present invention provides an expression vector comprising a nucleic acid molecule encoding the novel haemopoietin receptor or a derivative thereof as hereinbefore described, said expression vector capable of expression in a selected host cell.

Another aspect of the present invention contemplates a method for cloning a nucleotide sequence encoding NR6 or a derivative thereof, said method comprising searching a nucleotide data base for a sequence which encodes the amino acid sequence set forth in SEQ ID NO:1, designing one or more oligonucleotide primers based on the nucleotide sequence located in the search, screening a

nucleic acid library with said one or more oligonucleotides and obtaining a clone therefrom which encodes said NR6 or part thereof.

5 Once a novel nucleotide sequence is obtained as indicated above encoding NR6, oligonucleotides may be designed which bind cDNA clones with high stringency. Direct colony hybridisation may be employed or PCR amplification may be used. The use of oligonucleotide primers which bind under conditions of high stringency ensures rapid cloning of a molecule encoding the novel NR6 and less time is required in screening out cloning artefacts. However, depending on the primers used, low or medium stringency conditions may also be employed.

10
15 Alternatively, a library may be screened directly such as using oligonucleotides set forth in SEQ ID NO:7 or SEQ ID NO:8 or a mixture of both oligonucleotides may be used. In addition, one or more of oligonucleotides defined in SEQ ID NO:2 to 11 may also be used.

20
25 Preferably, the nucleic acid library is a cDNA, genomic, cDNA expression or mRNA library.

30
35 Preferably, the nucleic acid library is a cDNA expression library.

Preferably, the nucleotide data base is of human or murine origin and of brain, liver, kidney, neo-natal tissue, embryonic tissue, tumour or cancer tissue origin.

Preferred percentage similarities to the reference nucleotide sequences include at least about 70%, more preferably at least about 80%, still more preferably at least about 90% and even more preferably at least about 95% or above.

Another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haemopoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:13 or having at least about 50% similarity to all or part thereof.

Still yet another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haemopoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:15 or having at least about 50% similarity to all or part thereof.

Even yet another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haemopoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:17 or having at least about 50% similarity to all or part thereof.

A further aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haemopoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:19 or having at least about 50% similarity to all or part thereof.

Even yet another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haemopoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:25 or having at least about 50% similarity to all or part thereof.

Another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of

nucleotides encoding a novel haemopoietin receptor or derivative thereof having an amino acid sequence as set forth in one or more of SEQ ID NOS:29 or having at least about 50% similarity to all or part thereof.

5

Preferably, the percentage amino acid similarity is at least about 60%, more preferably at least about 70%, even more preferably at least about 80-85% and still even more preferably at least about 90-95% or greater.

10

The NR6 polypeptide contemplated by the present invention includes, therefore, derivatives which are components, parts, fragments, homologues or analogues of the novel haemopoietin receptors which are preferably encoded by all or part of a nucleotide sequences substantially set forth in SEQ ID NO:12 or 14 or 16 or 18 or 25 or 20 or 24 or 28 or 38 or a molecule having at least about 60% nucleotide similarity to all or part thereof or a molecule capable of hybridising to the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 20 or 24 or 28 or 38 or a complementary form thereof. The NR6 molecule may be glycosylated or non-glycosylated. When in glycosylated form, the glycosylation may be substantially the same as naturally occurring haemopoietin receptor or may be a modified form of glycosylation. Altered or differential glycosylation states may or may not affect binding activity of the novel receptor.

20

The NR6 haemopoietin receptor may be in soluble form or may be expressed on a cell surface or conjugated or fused to a solid support or another molecule.

30

As stated above, the present invention further contemplates a range of derivatives of NR6. Derivatives include fragments, parts, portions, mutants, homologues and analogues of the NR6 polypeptide and corresponding

genetic sequence. Derivatives also include single or multiple amino acid substitutions, deletions and/or additions to NR6 or single or multiple nucleotide substitutions, deletions and/or additions to the genetic sequence encoding NR6. "Additions" to amino acid sequences or nucleotide sequences include fusions with other peptides, polypeptides or proteins or fusions to nucleotide sequences. Reference herein to ANR6" includes reference to all derivatives thereof including functional derivatives or NR6 immunologically interactive derivatives.

Analogues of NR6 contemplated herein include, but are not limited to, modification to side chains, incorporating of unnatural amino acids and/or their derivatives during peptide, polypeptide or protein synthesis and the use of crosslinkers and other methods which impose conformational constraints on the proteinaceous molecule or their analogues.

Examples of side chain modifications contemplated by the present invention include modifications of amino groups such as by reductive alkylation by reaction with an aldehyde followed by reduction with NaBH₄; amidination with methylacetimidate; acylation with acetic anhydride; carbamoylation of amino groups with cyanate; trinitrobenzylolation of amino groups with 2, 4, 6-trinitrobenzene sulphonic acid (TNBS); acylation of amino groups with succinic anhydride and tetrahydronaphthalic anhydride; and pyridoxylation of lysine with pyridoxal-5-phosphate followed by reduction with NaBH₄.

The guanidine group of arginine residues may be modified by the formation of heterocyclic condensation products with reagents such as 2,3-butanedione, phenylglyoxal and glyoxal.

The carboxyl group may be modified by carbodiimide activation via O-acylisourea formation followed by subsequent derivitisation, for example, to a corresponding amide.

5

Sulphydryl groups may be modified by methods such as carboxymethylation with iodoacetic acid or iodoacetamide; performic acid oxidation to cysteic acid; formation of a mixed disulphides with other thiol compounds; reaction with maleimide, maleic anhydride or other substituted maleimide; formation of mercurial derivatives using 4-chloromercuribenzoate, 4-chloromercuriphenylsulphonic acid, phenylmercury chloride, 2-chloromercuri-4-nitrophenol and other mercurials; carbamoylation with cyanate at alkaline pH.

Tryptophan residues may be modified by, for example, oxidation with N-bromosuccinimide or alkylation of the indole ring with 2-hydroxy-5-nitrobenzyl bromide or sulphenyl halides. Tyrosine residues on the other hand, may be altered by nitration with tetranitromethane to form a 3-nitrotyrosine derivative.

25

Modification of the imidazole ring of a histidine residue may be accomplished by alkylation with iodoacetic acid derivatives or N-carbethoxylation with diethylpyrocarbonate.

30

Examples of incorporating unnatural amino acids and derivatives during peptide synthesis include, but are not limited to, use of norleucine, 4-amino butyric acid, 4-amino-3-hydroxy-5-phenylpentanoic acid, 6-aminohexanoic acid, t-butylglycine, norvaline, phenylglycine, ornithine, sarcosine, 4-amino-3-hydroxy-6-methylheptanoic acid, 2-thienyl alanine and/or D-isomers of amino acids. A list of unnatural amino acid, contemplated herein is shown in Table 1.

These types of modifications may be important to stabilise NR6 if administered to an individual or for use as a diagnostic reagent.

- 5 Crosslinkers can be used, for example, to stabilise 3D conformations, using homo-bifunctional crosslinkers such as the bifunctional imido esters having $(CH_2)_n$ spacer groups with n=1 to n=6, glutaraldehyde, N-hydroxysuccinimide esters and hetero-bifunctional
- 10 reagents which usually contain an amino-reactive moiety such as N-hydroxysuccinimide and another group specific-reactive moiety such as maleimido or dithio moiety (SH) or carbodiimide (COOH). In addition, peptides can be conformationally constrained by, for example,
- 15 incorporation of C" and N -methylamino acids, introduction of double bonds between C_α and C_β atoms of amino acids and the formation of cyclic peptides or analogues by introducing covalent bonds such as forming an amide bond between the N and C termini, between two
- 20 side chains or between a side chain and the N or C terminus.

TABLE 1

	Non-conventional amino acid	Code	Non-conventional amino acid	Code
5	aminobutyric acid	Abu	L-N-methylalanine	Nmala
	Amino-"-methylbutyrate	Mgabu	L-N-methylarginine	Nmarg
	aminocyclopropane- carboxylate	Cpro	L-N-methyleasparagine	Nmasn
			L-N-methyleaspartic acid	Nmasp
10	aminoisobutyric acid	Aib	L-N-methylcysteine	Nmcys
	aminonorbornyl- carboxylate	Norb	L-N-methylglutamine	Nmgln
	cyclohexylalanine		L-N-methylglutamic acid	Nmglu
	cyclopentylalanine	Cpen	Chexal-N-methylhistidine	Nmhis
15	D-alanine	Dal	L-N-methylleucine	Nmleu
	D-arginine	Darg	L-N-methyllysine	Nmlys
	D-aspartic acid	Dasp	L-N-methylmethionine	Nmmet
	D-cysteine	Dcys	L-N-methylnorleucine	Nmnle
	D-glutamine	Dgln	L-N-methylnorvaline	Nmnva
20	D-glutamic acid	Dglu	L-N-methylornithine	Nmorn
	D-histidine	Dhis	L-N-methylphenylalanine	Nmphe
	D-isoleucine	Dile	L-N-methylproline	Nmpro
	D-leucine	Dleu	L-N-methylserine	Nmser
	D-lysine	Dlys	L-N-methylthreonine	Nmthr
25	D-methionine	Dmet	L-N-methyltryptophan	Nmtrp
	D-ornithine	Dorn	L-N-methyltyrosine	Nmtyr
	D-phenylalanine	Dphe	L-N-methylvaline	Nmval
	D-proline	Dpro	L-N-methylethylglycine	Nmetg
	D-serine	Dser	L-N-methyl-t-butylglycine	Nmtbug
30	D-threonine	Dthr	L-norleucine	Nle
	D-tryptophan	Dtrp	L-norvaline	Nva
	D-tyrosine	Dtyr	"-methyl-aminoisobutyrate	Maib
	D-valine	Dval	"-methyl-(-aminobutyrate	Mgabu
	D-"-methylalanine	Dmala	"-methylcyclohexylalanine	Mchexa
35	D-"-methylarginine	Dmarg	"-methylcyclopentylalanine	Mcpen
	D-"-methylasparagine	Dmasn	"-methyl-"-napthylalanine	Manap
	D-"-methylaspartate	Dmasp	"-methylpenicillamine	Mpen

	D- ² -methylcysteine	Dmcys	N-(4-aminobutyl)glycine	Nglu
	D- ² -methylglutamine	Dmgln	N-(2-aminoethyl)glycine	Naeg
	D- ² -methylhistidine	Dmhis	N-(3-aminopropyl)glycine	Norn
	D- ² -methylisoleucine	Dmile	N-amino- ² -methylbutyrate	Nmaabu
5	D- ² -methylleucine	Dmleu	² -naphthalalanine	Anap
	D- ² -methyllysine	Dmlys	N-benzylglycine	Nphe
	D- ² -methylmethionine	Dmmet	N-(2-carbamylethyl)glycine	Ngln
	D- ² -methylornithine	Dmorn	N-(carbamylmethyl)glycine	Nasn
	D- ² -methylphenylalanine	Dmphe	N-(2-carboxyethyl)glycine	Nglu
	D- ² -methylproline	Dmpro	N-(carboxymethyl)glycine	Nasp
10	D- ² -methylserine	Dmser	N-cyclobutylglycine	Ncbut
	D ² -methylthreonine	Dmthr	N-cycloheptylglycine	Nchep
	D- ² -methyltryptophan	Dmtrp	N-cyclohexylglycine	Nchex
	D- ² -methyltyrosine	Dmty	N-cyclodecylglycine	Ncdec
	D- ² -methylvaline	Dmval	N-cyclododecylglycine	Ncdod
15	D-N-methylalanine	Dnmala	N-cyclooctylglycine	Ncoct
	D-N-methylarginine	Dnmarg	N-cyclopropylglycine	Ncprom
	D-N-methyleasparagine	Dnmasn	N-cycloundecylglycine	Ncund
	D-N-methyleaspartate	Dnmasp	N-(2,2-diphenylethyl)glycine	Nbhdm
	D-N-methylcysteine	Dnmcys	N-(3,3-diphenylpropyl)glycine	Nbhe
20	D-N-methylglutamine	Dnmgln	N-(guanidinopropyl)glycine	Narg
	D-N-methylglutamate	Dnmglu	N-(hydroxyethyl)glycine	Nthr
	D-N-methylhistidine	Dnmhis	N-(hydroxyethyl)glycine	Nser
	D-N-methylisoleucine	Dnmile	N-(imidazolyethyl)glycine	Nhis
	D-N-methylleucine	Dnmleu	N-(indolyllyethyl)glycine	Nhtrp
25	D-N-methyllysine	Dnmlys	N-methyl-(-aminobutyrate	Nmgabu
	N-methylcyclohexylalanine	Nmchexa	D-N-methylmethionine	Dnmmet
	D-N-methylornithine	Dnmorn	N-methylcyclopentylalanine	
	NmcpenN-methylglycine	Nala	D-N-methylphenylalanine	Dnmph
	N-methylaminoisobutyrate	Nmaib	D-N-methylproline	Dnmpro
30	N-(1-methylpropyl)glycine	Nile	D-N-methylserine	Dnmser
	N-(2-methylpropyl)glycine	Nieu	D-N-methylthreonine	Dnmthr
	D-N-methyltryptophan	Dnmtrp	N-(methylethyl)glycine	Nval
	D-N-methyltyrosine	Dnmtyr	N-methyla-naphthalalanine	Nmanap
	D-N-methylvaline	Dnmval	N-methylpenicillamine	Nmpen
35	(-aminobutyric acid	Gabu	N-(p-hydroxyphenyl)glycine	Nhtyr
	L-t-butylglycine	Tbug	N-(thiomethyl)glycine	Ncys

	L-ethylglycine	Etg	penicillamine	Pen
	L-homophenylalanine	Hphe	L-"-methylalanine	Mala
	L-"-methylarginine	Marg	L-"-methylasparagine	Masn
	L-"-methylaspartate	Masp	L-"-methyl-t-butylglycine	Mtbug
5	L-"-methylcysteine	Mcys	L-methylethylglycine	Metg
	L-"-methylglutamine	Mgln	L-"-methylglutamate	Mglu
	L-"-methylhistidine	Mhis	L-"-methylhomophenylalanine	Mhphe
	L-"-methylisoleucine	Mile	N-(2-methylthioethyl)glycine	Nmet
	L-"-methylleucine	Mleu	L-"-methyllysine	Mlys
10	L-"-methylmethionine	Mmet	L-"-methylnorleucine	Mnle
	L-"-methylnorvaline	Mnva	L-"-methylornithine	Morn
	L-"-methylphenylalanine	Mphe	L-"-methylproline	Mpro
	L-"-methylserine	Mser	L-"-methylthreonine	Mthr
	L-"-methyltryptophan	Mtrp	L-"-methyltyrosine	Mtyr
15	L-"-methylvaline	Mval	L-N-methylhomophenylalanine	Nmhphe
	N-(N-(2,2-diphenylethyl) carbamylmethyl)glycine	Nnbhm	N-(N-(3,3-diphenylpropyl) carbamylmethyl)glycine	Nnbhe
	1-carboxy-1-(2,2-diphenyl- Nmbo		ethylamino)cyclopropane	

20

The present invention further contemplates chemical analogues of NR6 capable of acting as antagonists or agonists of NR6 or which can act as functional analogues of NR6. Chemical analogues may not necessarily be derived from NR6 but may share certain conformational similarities. Alternatively, chemical analogues may be specifically designed to mimic certain physicochemical properties of NR6. Chemical analogues may be chemically synthesised or may be detected following, for example, natural product screening.

The identification of NR6 permits the generation of a range of therapeutic molecules capable of modulating expression of NR6 or modulating the activity of NR6. Modulators contemplated by the present invention includes agonists and antagonists of NR6 expression. Antagonists of NR6 expression include antisense

molecules, ribozymes and co-suppression molecules. Agonists include molecules which increase promoter ability or interfere with negative regulatory mechanisms. Agonists of NR6 include molecules which 5 overcome any negative regulatory mechanism. Antagonists of NR6 include antibodies and inhibitor peptide fragments.

Other derivatives contemplated by the present invention 10 include a range of glycosylation variants from a completely unglycosylated molecule to a modified glycosylated molecule. Altered glycosylation patterns may result from expression of recombinant molecules in different host cells.

15 Another embodiment of the present invention contemplates a method for modulating expression of NR6 in a subject such as a human or mouse, said method comprising contacting the genetic sequence encoding NR6 with an effective amount of a modulator of NR6 20 expression for a time and under conditions sufficient to up-regulate or down-regulate or otherwise modulate expression of NR6. Modulating NR6 expression provides a means of modulating NR6-ligand interaction or NR6 25 stimulation of cell activities.

Another aspect of the present invention contemplates a 30 method of modulating activity of NR6 in a human, said method comprising administering to said mammal a modulating effective amount of a molecule for a time and under conditions sufficient to increase or decrease NR6 activity. The molecule may be a proteinaceous molecule or a chemical entity and may also be a derivative of NR6 35 or its ligand or a chemical analogue or truncation mutant of NR6 or its ligand.

The present invention, therefore, contemplates a

pharmaceutical composition comprising NR6 or a derivative thereof or a modulator of NR6 expression or NR6 activity and one or more pharmaceutically acceptable carriers and/or diluents. These components are referred
5 to as the active ingredients.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions (where water soluble) and sterile powders for the extemporaneous preparation
10 of sterile injectable solutions. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dilution medium comprising, for
15 example, water, ethanol, polyol (for example, glycerol, propylene glycol and liquid polyethylene glycol, and the like), suitable mixtures thereof, and vegetable oils. The proper fluidity can be maintained, for example, by the use of surfactants. The preventions of the action
20 of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal and the like. In many cases, it will be preferable to include isotonic agents, for example,
25 sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

30 Sterile injectable solutions are prepared by incorporating the active compounds in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilization. In the case of
35 sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and the freeze-drying

technique which yield a powder of the active ingredient plus any additional desired ingredient from previously sterile-filtered solution thereof.

5 When the active ingredients are suitably protected they may be orally administered, for example, with an inert diluent or with an assimilable edible carrier, or it may be enclosed in hard or soft shell gelatin capsule, or it may be compressed into tablets, or it may be
10 incorporated directly with the food of the diet. For oral therapeutic administration, the active compound may be incorporated with excipients and used in the form of ingestible tablets, buccal tablets, troches, capsules, elixirs, suspensions, syrups, wafers, and the like.
15 Such compositions and preparations should contain at least 1% by weight of active compound. The percentage of the compositions and preparations may, of course, be varied and may conveniently be between about 5 to about 80% of the weight of the unit. The amount of active
20 compound in such therapeutically useful compositions in such that a suitable dosage will be obtained. Preferred compositions or preparations according to the present invention are prepared so that an oral dosage unit form contains between about 0.1 ug and 2000 mg of active
25 compound. Alternative dosage amounts include from about 1 Fg to about 1000 mg and from about 10 Fg to about 500 mg.

30 The tablets, troches, pills, capsules and the like may also contain the components as listed hereafter: A binder such as gum, acacia, corn starch or gelatin; excipients such as dicalcium phosphate; a disintegrating agent such as corn starch, potato starch, alginic acid and the like; a lubricant such as
35 magnesium stearate; and a sweetening agent such a sucrose, lactose or saccharin may be added or a flavouring agent such as peppermint, oil of wintergreen,

or cherry flavouring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar or both. A syrup or elixir may contain the active compound, sucrose as a sweetening agent, methyl and propylparabens as preservatives, a dye and flavouring such as cherry or orange flavour. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compound(s) may be incorporated into sustained-release preparations and formulations.

The present invention also extends to forms suitable for topical application such as creams, lotions and gels as well as a range of "paints" which are applied to skin and through which the active ingredients are absorbed.

Pharmaceutically acceptable carriers and/or diluents include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutical active substances is well known in the art and except insofar as any conventional media or agent is incompatible with the active ingredient, their use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units

suited as unitary dosages for the mammalian subjects to be treated; each unit containing a predetermined quantity of active material calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the novel dosage unit forms of the invention are dictated by and directly dependent on (a) the unique characteristics of the active material and the particular therapeutic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active material for the treatment of disease in living subjects having a diseased condition in which bodily health is impaired as herein disclosed in detail.

The principal active ingredient is compounded for convenient and effective administration in effective amounts with a suitable pharmaceutically acceptable carrier in dosage unit form as hereinbefore disclosed. A unit dosage form can, for example, contain the principal active compound in amounts ranging from 0.5 :g to about 2000 mg. Expressed in proportions, the active compound is generally present in from about 0.5 :g to about 2000 mg/ml of carrier. In the case of compositions containing supplementary active ingredients, the dosages are determined by reference to the usual dose and manner of administration of the said ingredients. Dosages may also be expressed per body weight of the recipient. For example, from about 10 ng to about 1000 mg/kg body weight, from about 100 ng to about 500 mg/kg body weight and for about 1 Fg to above 250 mg/kg body weight may be administered.

The pharmaceutical composition may also comprise genetic molecules such as a vector capable of transfecting target cells where the vector carries a nucleic acid molecule capable of modulating NR6 expression or NR6

activity. The vector may, for example, be a viral vector.

Still another aspect of the present invention is
5 directed to antibodies to NR6 and its derivatives. Such
antibodies may be monoclonal or polyclonal and may be
selected from naturally occurring antibodies to NR6 or
may be specifically raised to NR6 or derivatives
thereof. In the case of the latter, NR6 or its
10 derivatives may first need to be associated with a
carrier molecule. The antibodies and/or recombinant NR6
or its derivatives of the present invention are
particularly useful as therapeutic or diagnostic agents.
For example, NR6 antibodies or antibodies to its ligand
15 may act as antagonists.

For example, NR6 and its derivatives can be used to
screen for naturally occurring antibodies to NR6. These
may occur, for example in some autoimmune diseases.
20 Alternatively, specific antibodies can be used to screen
for NR6. Techniques for such assays are well known in
the art and include, for example, sandwich assays and
ELISA. Knowledge of NR6 levels may be important for
diagnosis of certain cancers or a predisposition to
25 cancers or for monitoring certain therapeutic protocols.

Antibodies to NR6 of the present invention may be
monoclonal or polyclonal. Alternatively, fragments of
antibodies may be used such as Fab fragments.
30 Furthermore, the present invention extends to
recombinant and synthetic antibodies and to antibody
hybrids. A "synthetic antibody" is considered herein to
include fragments and hybrids of antibodies. The
antibodies of this aspect of the present invention are
35 particularly useful for immunotherapy and may also be
used as a diagnostic tool for assessing apoptosis or
monitoring the program of a therapeutic regimen.

For example, specific antibodies can be used to screen for NR6 proteins. The latter would be important, for example, as a means for screening for levels of NR6 in a cell extract or other biological fluid or purifying NR6 made by recombinant means from culture supernatant fluid. Techniques for the assays contemplated herein are known in the art and include, for example, sandwich assays and ELISA.

It is within the scope of this invention to include any second antibodies (monoclonal, polyclonal or fragments of antibodies or synthetic antibodies) directed to the first mentioned antibodies discussed above. Both the first and second antibodies may be used in detection assays or a first antibody may be used with a commercially available anti-immunoglobulin antibody. An antibody as contemplated herein includes any antibody specific to any region of NR6.

Both polyclonal and monoclonal antibodies are obtainable by immunization with the enzyme or protein and either type is utilizable for immunoassays. The methods of obtaining both types of sera are well known in the art. Polyclonal sera are less preferred but are relatively easily prepared by injection of a suitable laboratory animal with an effective amount of NR6, or antigenic parts thereof, collecting serum from the animal, and isolating specific sera by any of the known immunoabsorbent techniques. Although antibodies produced by this method are utilizable in virtually any type of immunoassay, they are generally less favoured because of the potential heterogeneity of the product.

The use of monoclonal antibodies in an immunoassay is particularly preferred because of the ability to produce them in large quantities and the homogeneity of the product. The preparation of hybridoma cell lines for

monoclonal antibody production derived by fusing an immortal cell line and lymphocytes sensitized against the immunogenic preparation can be done by techniques which are well known to those who are skilled in the
5 art.

Another aspect of the present invention contemplates a method for detecting NR6 in a biological sample from a subject said method comprising contacting said
10 biological sample with an antibody specific for NR6 or its derivatives or homologues for a time and under conditions sufficient for an antibody-NR6 complex to form, and then detecting said complex.

The presence of NR6 may be accomplished in a number of ways such as by Western blotting and ELISA procedures.
15 A wide range of immunoassay techniques are available as can be seen by reference to US Patent Nos. 4,016,043, 4,424,279 and 4,018,653. These, of course, includes both single-site and two-site or "sandwich" assays of the
20 non-competitive types, as well as in the traditional competitive binding assays. These assays also include direct binding of a labelled antibody to a target.

Sandwich assays are among the most useful and commonly
25 used assays and are favoured for use in the present invention. A number of variations of the sandwich assay technique exist, and all are intended to be encompassed by the present invention. Briefly, in a typical forward assay, an unlabelled antibody is immobilized on a solid
30 substrate and the sample to be tested brought into contact with the bound molecule. After a suitable period of incubation, for a period of time sufficient to allow formation of an antibody-antigen complex, a second antibody specific to the antigen, labelled with a
35 reporter molecule capable of producing a detectable signal is then added and incubated, allowing time sufficient for the formation of another complex of

antibody-antigen-labelled antibody. Any unreacted material is washed away, and the presence of the antigen is determined by observation of a signal produced by the reporter molecule. The results may either be
5 qualitative, by simple observation of the visible signal, or may be quantitated by comparing with a control sample containing known amounts of hapten. Variations on the forward assay include a simultaneous assay, in which both sample and labelled antibody are
10 added simultaneously to the bound antibody. These techniques are well known to those skilled in the art, including any minor variations as will be readily apparent. In accordance with the present invention, the sample is one which might contain NR6 including cell
15 extract, tissue biopsy or possibly serum, saliva, mucosal secretions, lymph, tissue fluid and respiratory fluid. The sample is, therefore, generally a biological sample comprising biological fluid but also extends to fermentation fluid and supernatant fluid such as from a
20 cell culture.

In the typical forward sandwich assay, a first antibody having specificity for the NR6 or antigenic parts thereof, is either covalently or passively bound to a solid surface. The solid surface is typically glass or a polymer, the most commonly used polymers being cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene. The solid supports may be in the form of tubes, beads, discs of microplates, or any
25 other surface suitable for conducting an immunoassay. The binding processes are well-known in the art and generally consist of cross-linking covalently binding or physically adsorbing, the polymer-antibody complex is washed in preparation for the test sample. An aliquot
30 of the sample to be tested is then added to the solid phase complex and incubated for a period of time sufficient (e.g. 2-40 minutes or overnight if more
35

convenient) and under suitable conditions (e.g. from about room temperature to about 37°C) to allow binding of any subunit present in the antibody. Following the incubation period, the antibody subunit solid phase is washed and dried and incubated with a second antibody specific for a portion of the hapten. The second antibody is linked to a reporter molecule which is used to indicate the binding of the second antibody to the hapten.

An alternative method involves immobilizing the target molecules in the biological sample and then exposing the immobilized target to specific antibody which may or may not be labelled with a reporter molecule. Depending on the amount of target and the strength of the reporter molecule signal, a bound target may be detectable by direct labelling with the antibody. Alternatively, a second labelled antibody, specific to the first antibody is exposed to the target-first antibody complex to form a target-first antibody-second antibody tertiary complex. The complex is detected by the signal emitted by the reporter molecule.

In another alternative method, the NR6 ligand is immobilised to a solid support and a biological sample containing NR6 brought into contact with its immobilised ligand. Binding between NR5 and its ligand can then be determined using an antibody to NR6 which itself may be labelled with a reporter molecule or a further anti-immunoglobulin antibody labelled with a reporter molecule could be used to detect antibody bound to NR6.

By "reporter molecule" as used in the present specification, is meant a molecule which, by its chemical nature, provides an analytically identifiable signal which allows the detection of antigen-bound antibody. Detection may be either qualitative or

quantitative. The most commonly used reporter molecules in this type of assay are either enzymes, fluorophores or radionuclide containing molecules (i.e. radioisotopes) and chemiluminescent molecules.

5 In the case of an enzyme immunoassay, an enzyme is conjugated to the second antibody, generally by means of glutaraldehyde or periodate. As will be readily recognized, however, a wide variety of different conjugation techniques exist, which are readily

10 available to the skilled artisan. Commonly used enzymes include horseradish peroxidase, glucose oxidase, beta-galactosidase and alkaline phosphatase, amongst others. The substrates to be used with the specific enzymes are generally chosen for the production, upon hydrolysis by

15 the corresponding enzyme, of a detectable colour change. Examples of suitable enzymes include alkaline phosphatase and peroxidase. It is also possible to employ fluorogenic substrates, which yield a fluorescent product rather than the chromogenic substrates noted

20 above. In all cases, the enzyme-labelled antibody is added to the first antibody hapten complex, allowed to bind, and then the excess reagent is washed away. A solution containing the appropriate substrate is then added to the complex of antibody-antigen-antibody. The

25 substrate will react with the enzyme linked to the second antibody, giving a qualitative visual signal, which may be further quantitated, usually spectrophotometrically, to give an indication of the amount of hapten which was present in the sample.

30 "Reporter molecule" also extends to use of cell agglutination or inhibition of agglutination such as red blood cells on latex beads, and the like.

35 Alternately, fluorescent compounds, such as fluorescein and rhodamine, may be chemically coupled to antibodies without altering their binding capacity. When activated by illumination with light of a particular wavelength,

the fluorochrome-labelled antibody adsorbs the light energy, inducing a state to excitability in the molecule, followed by emission of the light at a characteristic colour visually detectable with a light microscope. As in the EIA, the fluorescent labelled antibody is allowed to bind to the first antibody-hapten complex. After washing off the unbound reagent, the remaining tertiary complex is then exposed to the light of the appropriate wavelength the fluorescence observed indicates the presence of the hapten of interest.

Immunofluorescence and EIA techniques are both very well established in the art and are particularly preferred for the present method. However, other reporter molecules, such as radioisotope, chemiluminescent or bioluminescent molecules, may also be employed.

The present invention also contemplates genetic assays such as involving PCR analysis to detect the NR6 gene or its derivatives. Alternative methods or methods used in conjunction include direct nucleotide sequencing or mutation scanning such as single stranded conformational polymorphisms analysis (SSCP) as specific oligonucleotide hybridisation, as methods such as direct protein truncation tests.

The nucleic acid molecules of the present invention may be DNA or RNA. When the nucleic acid molecule is in a DNA form, it may be genomic DNA or cDNA. RNA forms of the nucleic acid molecules of the present invention are generally mRNA.

Although the nucleic acid molecules of the present invention are generally in isolated form, they may be integrated into or ligated to or otherwise fused or associated with other genetic molecules such as vector molecules and in particular expression vector molecules. Vectors and expression vectors are generally capable of

replication and, if applicable, expression in one or both of a prokaryotic cell or a eukaryotic cell. Preferably, prokaryotic cells include *E. coli*, *Bacillus* sp and *Pseudomonas* sp. Preferred eukaryotic cells 5 include yeast, fungal, mammalian and insect cells.

Accordingly, another aspect of the present invention contemplates a genetic construct comprising a vector portion and a mammalian and more particularly a human 10 NR6 gene portion, which NR6 gene portion is capable of encoding an NR6 polypeptide or a functional or immunologically interactive derivative thereof.

Preferably, the NR6 gene portion of the genetic 15 construct is operably linked to a promoter on the vector such that said promoter is capable of directing expression of said NR6 gene portion in an appropriate cell.

20 In addition, the NR6 gene portion of the genetic construct may comprise all or part of the gene fused to another genetic sequence such as a nucleotide sequence encoding maltose binding protein or glutathione-S-transferase or part thereof.

25 The present invention extends to such genetic constructs and to prokaryotic or eukaryotic cells comprising same.

30 The present invention also extends to any or all derivatives of NR6 including mutants, part, fragments, portions, homologues and analogues or their encoding genetic sequence including single or multiple nucleotide or amino acid substitutions, additions and/or deletions to the naturally occurring nucleotide or amino acid 35 sequence.

NR6 may be important for the proliferation,

differentiation and survival of a diverse array of cell types. Accordingly, it is proposed that NR6 or its functional derivatives be used to regulate development, maintenance or regeneration in an array of different 5 cells and tissues *in vitro* and *in vivo*. For example, NR6 is contemplated to be useful in modulating neuronal proliferation, differentiation and survival.

10 Soluble NR6 polypeptides are also contemplated to be useful in the treatment of a range of diseases, injuries or abnormalities.

15 Membrane bound or soluble NR6 may be used *in vitro* on nerve cells or tissues to modulate proliferation, differentiation or survival, for example, in grafting procedures or transplantation.

20 As stated above, the NR6 of the present invention or its functional derivatives may be provided in a pharmaceutical composition comprising the NR6 together with one or more pharmaceutically acceptable carriers and/or diluents. In addition, the present invention contemplates a method of treatment comprising the administration of an effective amount of a NR6 of the 25 present invention. The present invention also extends to antagonists and agonists of NR6s and their use in therapeutic compositions and methodologies.

30 A further aspect of the present invention contemplates the use of NR6 or its functional derivatives in the manufacture of a medicament for the treatment of NR6 mediated conditions defective or deficient.

35 Still a further aspect of the present invention contemplates a ligand for NR6 preferably, in isolated or recombinant form or a derivative of said ligand.

The present invention further contemplates knockout animals such as mice or other murine species for the NR6 gene including homozygous and heterozygous knockout animals. Such animals provide a particularly useful 5 live in vivo model for studying the effects of NR6 as well as screening for agents capable of acting as agonists or antagonists of NR6.

According to this embodiment there is provided a 10 transgenic animal comprising a mutation in at least one allele of the gene encoding NR6. Additionally, the present invention provides a transgenic animal comprising a mutation in two alleles of the gene encoding NR6. Preferably, the transgenic animal is a 15 murine animal such as a mouse or rat.

The present invention is further described by the following non-limiting Figures and Examples.

20 In the Figures:

Figure 1 is a diagrammatic representation showing expansion of sequenced region of the mouse NR6 gene indicating splicing patterns seen in the three forms of 25 NR6 cDNA, NR6.1, NR6.2 and NR6.3.

Figure 2 is a representation of the nucleotide sequence of the mouse NR6 gene, containing exons encoding the cDNA from nucleotide 148 encoding D50 of the cDNAs shown 30 in SEQ ID NOS:12 and 14 to the end of the 3N untranslated region shared by both NR6.1, NR6.2 and NR6.3. In this figure, this region encompasses nucleotides g1182 to g6617. This sequence is also defined in SEQ ID NO:28.

35

Figure 3 is a representation of the nucleotide sequence of the mouse genomic NR6 gene with additional 5N

sequences. The coding exons of NR6 span approximately 11kb of the mouse genome. There are 9 coding exons separated by 8 introns:

	exon1	at least 239nt	intron1	5195nt
5	exon 2	282nt	intron2	214nt
	exon3	130nt	intron3	107nt
	exon4	170nt	intron4	1372nt
	exon5	158nt	intron5	68nt
	exon6	169nt	intron6	2020nt
10	exon6	188nt	intron7	104nt
	exon8	43nt	intron8	181nt
	exon9	252nt		

Exon 1 encoding the signal sequence, exon 2 the Ig-like domain, exons 3 to 6 the hemopoietin domain. Exons 7, 8 and 9 are alternatively spliced.

Figure 4 is a diagrammatic representation showing the genomic structure of murine NR-6.

20

Figure 5 is a diagrammatic representation showing targetting of the NR6 locus by homologous recombination.

Single and three letter abbreviations for amino acid residues used in the specification are summarised in Table 2:

5

TABLE 2

	Amino Acid	Three-letter Abbreviation	One-letter Symbol
10	Alanine	Ala	A
	Arginine	Arg	R
	Asparagine	Asn	N
	Aspartic acid	Asp	D
	Cysteine	Cys	C
15	Glutamine	Gln	Q
	Glutamic acid	Glu	E
	Glycine	Gly	G
	Histidine	His	H
	Isoleucine	Ile	I
20	Leucine	Leu	L
	Lysine	Lys	K
	Methionine	Met	M
	Phenylalanine	Phe	F
	Proline	Pro	P
25	Serine	Ser	S
	Threonine	Thr	T
	Tryptophan	Trp	W
	Tyrosine	Tyr	Y
	Valine	Val	V
30	Any residue	Xaa	X

TABLE 3
SUMMARY OF SEQ ID NO.

Sequence	SEQ ID NO.
5 Amino acid sequence WSXWS	1
Oligonucleotide primers and probes listed in Example 1	2-11
Nucleotide sequence of NR6.1 ¹	12
Amino acid sequence of NR6.1	13
10 Nucleotide sequence of NR6.2 ²	14
Amino acid sequence of NR6.2	15
Nucleotide sequence of NR6.3 ³	16
Amino acid sequence of NR6.3	17
Nucleotide sequence of products generated by 5N RACE of brain cDNA using NR6 specific primers ⁴	18
Amino acid sequence of SEQ ID NO:18	19
Nucleotide sequence unique to 5N RACE of brain cDNA	20
20 Amino acid sequence for SEQ ID NO:20	21
Unspliced murine NR6 nucleotide sequence	22
PCR product for human NR6	23
Nucleotide sequence of clone HFK-66 encoding human NR6	24
25 Amino acid sequence of SEQ ID NO:24	25
Oligonucleotide sequences UP1 and LP1, respectively	26-27
Genomic nucleotide sequence of murine NR6	28
Amino acid sequence of SEQ ID NO:28	29
30 Murine NR6.1 oligonucleotide primers	30, 31
Murine IL-3 signal sequence	32
Linker sequence for mouse IL-3 signal sequence and FLAG epitope	33-35
Genomic nucleotide sequence of murine NR6 containing additonal 5N sequence	38
35 Oligonucleotide 2199 and 2200, respectively	36, 37
N-terminal region of NR6	39

¹The polyadenylation signal AATAAATAAA is at nucleotide position 1451 to 1460; NR6.1 (SEQ ID NO:12) and NR6.2 (SEQ ID NO:14) are identical to nucleotide 1223 encoding Q407, the represents the end of an exon. NR6.1 splices 5 out an exon present only in NR6.2 and uses a different reading frame for the final exon which is shared with NR6.2; this corresponds to amino acids VLPAKL at amino acid residue positions 408-413. The region of 3N- untranslated DNA shared by NR6.1, NR6.2 and NR6.3 is 10 from nucleotide 1240 to 1475. The WSXWS motif is at amino acid residues 330 to 334.

²The polyadenylation signal AATAAA is at nucleotide positions 1494 to 1503. The WSXWS motif is at amino 15 acid residues 330 to 334. NR6.1 and NR6.2 are identical to nucleotide 1223 encoding Q407 which represents the end of an exon. NR6.2 splices in an exon beginning at amino acid residue D408, nucleotide 1224 and ends at residue G422, nucleotide 1264. The region of 3N 20 untranslated DNA shared by NR6.1, NR6.2 and NR6.3 is from nucleotide position 1283 to 1517.

³The nucleotide and amino acid numbering corresponds to SEQ ID NO:12 and 14. The WSXWS motif is at amino acid 25 residues 330 to 334. The polyadenylation signal AATAAATAAA is from nucleotide 1781 to 1780. NR6.1, NR6.2 and NR6.3 are identical to nucleotide 1223 encoding Q407, this represents the end of an exon. NR6.3 fails to splice from this position and, therefore, 30 translation continues through the intron, giving rise to the C-terminal protein region from amino acid residues 408 to 461. The region of 3N untranslated DNA shared by NR6.1, NR6.2 and NR6.3 is from nucleotide 1469 to 1804.

35 ⁴The nucleotide sequence is identical to NR6.1, NR6.2 and NR6.3 from nucleotide C151, the first nucleotide for Pro51. The numbering from this nucleotide is the same

as for SEQ ID NO:14 and 16. The 5N of this point is unique to the products generated by 5N RACE not being found in NR6.1, NR6.2 and NR6.3 and is represented in SEQ ID NOS:20 and 21.

5

⁵Structure of the murine genomic NR6 locus. The coding exons of NR6 span approximately 11kb of the mouse genome. There are 9 coding exons separated by 8 introns:

10

exon 1	at least 239nt	intron1	5195nt
exon 2	282nt	intron2	214nt
exon 3	130nt	intron3	107nt
exon 4	170nt	intron 4	1372nt
15 exon 5	158nt	intron5	68nt
exon 6	169nt	intron6	2020nt
exon 7	188nt	intron7	104nt
exon 8	43nt	intron8	181nt
exon 9	252nt		

20

Exon 1 encodes the signal sequence, exon 2 the Ig-like domain, exons 3 to 6 the hemopoietin domain. Exons 7, 8 and 9 are alternatively spliced.

25

The NRG molecules of the present invention have a range of utilities referred to in the subject specification. Additional utilities include:

1. Identification of molecules that interact with NR6.

30 These may include :

a) a corresponding ligand using standard orphan receptor techniques (26),

35 b) monoclonal antibodies that act either as receptors antagonists or agonists,

- c) mimetic or antagonistic peptides isolated using phage display technology (27,28),
 - d) small molecule natural products that act either as antagonists or agonists.
- 5

2. Development of diagnostics to detect deletions/rearrangements in the NR6 gene. The NR6 knock-out mice studies described herein provide a useful model for this utility. There are also applications in the field of reproduction. For example, people can be tested for their NR6 status. NR6 +/- carriers might be expected to give rise to offspring with developmental problems.

10

EXAMPLE 1

Oligonucleotides

	M116:	5' ACTCGCTCCAGATTCCCGCCTTTT 3'	[SEQ ID NO:2]
5	M108:	5' TCCCGCCTTTTCGACCCATAGAT 3'	[SEQ ID NO:3]
	M159:	5' GGTACTTGGCTTGGAAAGAGGAAAT 3'	[SEQ ID NO:4]
	M242:	5' CGGCTCACGTGCACGTCGGGTGGG 3'	[SEQ ID NO:5]
	M112:	5' AGCTGCTGTTAAAGGGCTTCTC 3'	[SEQ ID NO:6]
	WSDWS	5' (A/G) CTCCA (A/G) TC (A/G) CTCCA 3'	[SEQ ID NO:7]
10	WSEWS	5' (A/G) CTCCA (C/T) TC (A/G) CTCCA 3'	[SEQ ID NO:8]
	1944	5' AAGTGTGACCATCATGTGGAC 3'	[SEQ ID NO:9]
	2106	5' GGAGGTGTTAAGGAGGCG 3'	[SEQ ID NO:10]
	2120	5' ATGCCCGCGGGTCGCCCG 3'	[SEQ ID NO:11]

15 EXAMPLE 2

Isolation of initial NR6 cDNA clones using oligonucleotides designed against the conserved WSXWS motif found in members of the haemopoietin receptor family

20
(i) A commercial adult mouse testis cDNA library cloned
into the UNI-ZAP bacteriophage (Stratagene, CA, USA;
Catalogue numbers 937 308) was used to infect
Escherichia coli of the strain LE392. Infected bacteria
25 were grown on twenty 150 mm agar plates, to give
approximately 50,000 plaques per plate. Plaques were
then transferred to duplicate 150 mm diameter nylon
membranes (Colony/Plaque Screen, NEN Research Products,
MA, USA), bacteria were lysed and the DNA was denatured
30 and fixed by autoclaving at 100°C for 1 min with dry
exhaust. The filters were rinsed twice in 0.1% (w/v)
sodium dodecyl sulfate (SDS), 0.1 x SSC (SSC is 150 mM
sodium chloride, 15 mM sodium citrate dihydrate) at room
temperature and pre-hybridized overnight at 42°C in 6 x
35 SSC containing 2 mg/ml bovine serum albumin, 2 mg/ml
Ficoll, 2 mg/ml polyvinylpyrrolidone, 100 mM ATP, 10
mg/ml tRNA, 2 mM sodium pyrophosphate, 2 mg/ml salmon

sperm DNA, 0.1% (w/v) SDS and 200 mg/ml sodium azide. The pre-hybridisation buffer was removed. 1.2 Fg of the degenerate oligonucleotides for hybridization (WSDWS; Example 1) were phosphorylated with T4 polynucleotide kinase using 960 mCi of $\gamma^{32}\text{P}$ -ATP (Bresatec, S.A., Australia). Unincorporated ATP was separated from the labelled oligonucleotide using a pre-packed gel filtration column (NAP-5; Pharmacia, Uppsala, Sweden). Filters were hybridized overnight at 42°C in 80 ml of the prehybridisation buffer containing 0.1% (w/v) SDS, rather than NP40, and 10^6 - 10^7 cpm/ml of labelled oligonucleotide. Filters were briefly rinsed twice at room temperature in 6 x SSC, 0.1% (v/v) SDS, twice for 30 min at 45°C in a shaking waterbath containing 1.5 l of the same buffer and then briefly in 6 x SSC at room temperature. Filters were then blotted dry and exposed to autoradiographic film at -70°C using intensifying screens, for 7 - 14 days prior to development.

Plaques that appeared positive on orientated duplicate filters were picked, eluted in 1 ml of 100 mM NaCl, 10 mM MgCl₂, 10 mM Tris.HCl pH7.4 containing 0.5% (w/v) gelatin and 0.5% (v/v) chloroform and stored at 4°C. After 2 days LE392 cells were infected with the eluate from the primary plugs and replated for the secondary screen. This process was repeated until hybridizing plaques were pure.

Once purified, positive cDNAs were excised from the ZAP II bacteriophage according to the manufacturer's instructions (Stratagene, CA, USA) and cloned into the plasmid pBluescript. A CsCl purified preparation of the DNA was made and this was sequenced on both strands. Sequencing was performed using an Applied Biosystems automated DNA sequencer, with fluorescent dideoxynucleotide analogues according to the manufacturer's instructions. The DNA sequence was analysed using software supplied by Applied Biosystems.

Two clones isolated from the mouse testis cDNA library shared large regions of nucleotide sequence identity 68-1 and 68-2 and appeared to encode a novel member of the haemopoietin receptor family and the inventors gave the 5 putative receptor the working name "NR6".

(ii) In a parallel series of experiments, a commercial mouse brain cDNA library (STRATAGENE #967319, Balb/c day-20, whole brain cDNA/Uni-ZAP XR Vector) was used to 10 infect *E.coli* strain XL1-Blue MRF=. Infected bacteria were grown on 90x135mm square agar plates to give about 25,000 plaques per plate. Plaques were then transferred to positively charged nylon membranes, Hybond-N(+) (Amersham RPN 203B), bacteria were lysed and the DNA was 15 denatured with denaturing 0.5 M NaOH, 1.5 M NaCl at room temperature for 7 min. The membranes were neutralized with 0.5 M Tris-HCL pH7.2, 1.5 M NaCl, 1 mM EDTA at room temperature for 10 min before the DNA fixation by UV crosslinking.

20 A mixture of WSDWS and WSEWS oligonucleotide probes (SEQ ID NOS: 7 and 8) were labelled with a $[{}^{-32}\text{P}]$ -ATP (TOYOBO #PNK-104 Kination kit). The membranes from the mouse brain cDNA library were then hybridized with the 25 mixture of WSDWS and WSEWS oligonucleotide probes in the Rapid Hybridization Buffer (Amersham, RPN1636) at 42°C for 16 hours. Filters were washed with 1xSSC/0.1% (w/v) SDS at 42°C before autoradiography. Plaques that appeared positive on orientated duplicate filters were 30 picked and replated on *E. coli*, XL1-Blue MRFN with the process of immobilisation on nylon membranes, hybridization of membranes with oligonucleotide probes, washing and autoradiography repeated until pure plaques had been obtained.

35 The cDNA fragment from pure positively hybridizing plaques was isolated by excision with the helper phage

strain ExAssist according to the manufacturer=s instructions (Stratagene, #967319). Sequencing was performed after the amplification with Ampli-Taq DNA polymerase and Taq dideoxy terminator cycle sequencing kit (Perkin Elmer, #401150) by 25 cycles of 96°C for 10 sec, 50°C for 5 sec, 60°C for 4 min followed by 60°C for 5 min with the sequencing primers on an ABI model 377 DNA sequencer.

One clone, MBC-8, from the mouse brain library shared large regions of nucleotide sequence identity with both the 68-1 and 68-2 clones isolated from the mouse testis cDNA library.

(iii) In a third series of experiments, total RNA was prepared from the mouse osteoblastic cell line, KUSA, according to the method of Chirgwin et al. (15), and poly(A)+RNA was further purified by oligo(dT)-cellulose chromatography (Pharmacia Biotech). Complementary DNA was synthesized by oligo(dT) priming, inserted into the UniZAP XR directional cloning vector (Stratagene), and packaged into 8 phage using Gigapack Gold (Stratagene), yielding 1.25×10^7 independent clones.

Approximately 10^6 clones were screened essentially as described in (ii) above. Briefly, probes were labeled with ^{32}P using T4 polynucleotide kinase and prehybridization was performed for 4 hr in the Rapid hybridization buffer (Amersham LIFE SCIENCE) at 42°C. Filters (Hybond N+, Amersham) were then hybridized for 19 hr under the same condition with the addition of ^{32}P -labeled WSXWS mix oligonucleotides and washed 3 times. The final wash was for 30 min in 1 x SSPE, 0.1% (w/v) SDS at 42°C. Filters were then exposed with an intensifying screen to Kodak X-OMAT AR film for 5 days.

Isolated clones were subjected to the *in vivo* excision

of pBluescript SK(-) phagemid (Stratagene), and plasmid DNA was prepared by the standard method. DNA sequences were determined using an ABI PRISM 377 DNA Sequencer (Perkin Elmer) with appropriate synthetic oligonucleotide primers. A clone pKUSA166 shared large regions of nucleotide sequence identity with the MBC-8, 68-1 and 68-2 clones isolated from the mouse brain and testis cDNA libraries.

10

EXAMPLE 3**Isolation of further NR6 cDNA clones using probes specific for NR6**

(i) In order to identify other cDNA libraries containing cDNA clones for NR6, the inventors performed PCR upon 1 μ l aliquots of λ -bacteriophage cDNA libraries made from mRNA from various human tissues and using oligonucleotides 2070 and 2057, designed from the sequence of 68-1 and 68-2, as primers. Reactions contained 5 μ l of 10 x concentrated PCR buffer (Boehringer Mannheim GmbH, Mannheim, Germany), 1 μ l of 10 mM dATP, dCTP, dGTP and dTTP, 2.5 μ l of the oligonucleotides HYB2 and either T3 or T7 at a concentration of 100 mg/ml, 0.5 μ l of Taq polymerase (Boehringer Mannheim GmbH) and water to a final volume of 50 μ l. PCR was carried out in a Perkin-Elmer 9600 by heating the reactions to 96°C for 2 min and then for 25 cycles at 96°C for 30 sec, 55°C for 30 sec and 72°C for 2 min. PCR products were resolved on an agarose gel, immobilized on a nylon membrane and hybridized with 32 P-labelled oligonucleotide 1943 (SEQ ID NO:42).

In addition to the original library, a mouse brain cDNA library appeared to contain NR6 cDNAs. These were screened using a 32 P-labelled oligonucleotides 1944, 2106, 2120 (Example 1) or with a fragment of the original NR6 cDNA clone from 68-1 (nucleotide 934 to the

end of NR6.1 in Figure 1) labelled with ^{32}P using a random decanucleotide labelling kit (Bresatec). Conditions used were similar to those described in (i) above except that for the labelled oligonucleotides, 5 filters were washed at 55°C rather than 45°C, while for the NR6 cDNA fragment prehybridization and hybridization was carried out in 2xSSC and filters were washed at 0.2 x SSC at 65°C. Again, as described in (i) above, positively hybridising plaques were purified, the cDNAs 10 were recovered and cloned into plasmids pBluescript II or pUC19. Independent cDNA clones were sequenced on both strands.

Using this procedure, 6 further clones, 68-5, 68-35, 68-15 41, 68-51, 68-77 and 73-23, contained large regions of sequence identity with 68-1, 68-2, MBC-8 and pKUSA166.

In a parallel series of experiments, further screening 20 was performed with hybridization probes prepared from the 1.7 kbp EcoRI-XhoI fragment excised from pKUSA166. This fragment was excised and labeled with ^{32}P by using T7QuickPrime Kit (Pharmacia Biotech). Approximately 6 $\times 10^5$ clones were screened. Hybond N+ filters (Amersham) were first prehybridized for 4hr at 42°C in 25 50% (v/v) formamide, 5xSSPE, 5xDenhardt's solution, 0.1% (w/v) SDS, and 0.1mg/ml denatured salmon sperm DNA. Hybridization was for 16 hours under the same conditions with the addition of ^{32}P - labelled NR6- cDNA fragment probes. Finally the filters were washed once for 1hr in 30 0.2xSSC, 0.1% (w/v) SDS at 68°C. Eight clones were isolated, and phage clones were subjected to the *in vivo* excision of the pBluescript SK(-) phagemid (Stratagene). The plasmid DNAs were prepared by the standard method. 35 DNA sequences were determined by an ABI PRISM 377 DNA Sequencer using appropriate synthetic oligonucleotide primers.

Using this procedure 8 further clones from the KUSA library contained large regions of sequence identity with 68-1, 68-2, MBC-8, pKUSA166, 68-5, 68-35, 68-41, 68-51, 68-77 and 73-23 were isolated.

5

EXAMPLE 4**Isolation of genomic DNA encoding NR6**

DNA encoding the murine NR6 genomic locus was also
10 isolated using the 68-1 cDNA as a probe. Two positive
clones, 2-2 and 57-3, were isolated from a mouse 129/Sv
strain genomic DNA library cloned into λ FIX. These
clones were overlapping and the position of the
restriction sites, introns and exons were determined in
15 the conventional manner. The region of the genomic
clones containing exons and the intervening introns were
sequenced on both strands using an Applied Biosystems
automated DNA sequencer, with fluorescent
dideoxynucleotide analogues according to the
20 manufacturer's instructions. Figure 2 shows the
nucleotide sequence and corresponding amino acid
sequence of the translation regions. This is also shown
in SEQ ID NOs:30 and 31. Figure 3 provides the genomic
NR6 gene sequence but with additional 5'N sequence. This
25 is also represented in SEQ ID NO:38 in relation to this
sequence. The coding exons of NR6 span approximately
11kb of the mouse genome. There are 9 coding exons
separated by 8 introns:

30	exon1	at least 239nt	intron1	5195nt
	exon2	282nt	intron2	214nt
	exon3	130nt	intron3	107nt
	exon4	170nt	intron4	1372nt
	exon5	158nt	intron5	68nt
35	exon6	169nt	intron6	2020nt
	exon7	188nt	intron7	104nt
	exon8	43nt	intron8	181nt

exon9 252nt

Exon 1 encodes the signal sequence, exon 2 the Ig-like domain, exons 3 to 6 the hemopoietin domain. Exons 7, 8
5 and 9 are alternatively spliced.

EXAMPLE 5

10 **SN RACE analysis of NR6**

5'-RACE was used to investigate the nature of the sequence 5' of nucleotide 960, encoding Ile321 of NR6.1,
2 and 3. The nucleotide and corresponding amino acid
15 sequences are shown in SEQ ID NOs:12, 14 and 16,
respectively. 5'-RACE was performed using Advantage
KlenTaq polymerase (CLONTECH, CAT NO. K1905-1) on mouse
brain Marathon-ready cDNA (CLONTECH, CAT NO. 7450-1)
according to the manufacturer's instructions. Briefly,
20 the first rounds of amplification were performed using
5 μ l of cDNA in a total volume of 50 μ l, with 1mM each of
the primers AP1&M116 [SEQ ID NO:2] or AP1&M159 [SEQ ID
NO:4] by 35 cycles of 94°C x 0.5min, 68°C x 2.0min on
GeneAmp 2400 (Perkin-Elmer). An amount of 5 μ l of 50-
25 fold diluted product from the first amplification was
then re-amplified ; for the products generated with
primers AP1 and M116 [SEQ ID NO:2] in the first
amplification, 1 mM of the primers AP2&M108 [SEQ ID
NO:3] were used in the second amplification. For the
30 products generated with primers AP1 and M116 [SEQ ID
NO:2] in the first amplification, two separate secondary
reactions were performed, one reaction with 1 mM primers
AP2&M242 [SEQ ID NO:5] and the other with 1 mM primers
AP2&M112 [SEQ ID NO:6]. Amplification was achieved
35 using 25 cycles of 94°C x 0.5min, 68°C x 2.0min. These
samples were analyzed by agarose gel electrophoresis.
When a single ethidium bromide staining amplification

product was observed, it was purified by QIAquick PCR purification kit according to the manufacturer=s instructions (QIAGEN, CAT NO. DG-0281) and its sequence was directly determined using both primers used in the secondary amplification step, that is AP2 and either M108 [SEQ ID NO:3], M242 [SEQ ID NO:5] or M112 [SEQ ID NO:6].

EXAMPLE 6

From the initial screens of mouse brain and testis cDNA libraries with the degenerate WSXWS oligonucleotides and subsequent screening of cDNA libraries from mouse testis, mouse brain and the KUSA osteoblastic cells line a total of 18 NR6 cDNAs have been isolated. Nucleotide sequence of NR6 was also determined from 5'RACE analysis of brain cDNA. Additionally, two murine genomic DNA clones encoding NR6 have also been isolated.

20 Comparison of the NR6 cDNA clones revealed a common
region of nucleotide sequence which included a 123 base
pairs 5'-untranslated region and 1221 base pairs open
reading frame, stretching from the putative initiation
25 methionine, Met1 to Gln407 (SEQ ID NOs:12, 14 and 16,
respectively). Within this common open reading frame, a
haemopoietin receptor domain was observed which
contained the four conserved cysteine residues and the
five amino acid motif WSXWS typical of members of the
30 haemopoietin receptor family, was observed.

Further analyses revealed that after nucleotide 1221, three different classes of NR6 cDNAs could be found, these were termed NR6.1, NR6.2 and NR6.3 (SEQ ID NOS:12, 14 and 16, respectively). Each encoded a receptor that appeared to lack a classical transmembrane domain and, would, therefore be likely to be secreted into the

extracellular environment. Although the putative C-terminal region of the three classes of NR6 proteins appear to be different, the cDNAs encoding them also had a common region of 3'-untranslated region.

5

With regard to SEQ ID NOs:12, 14 and 16, the number of both nucleotides and amino acids begins at the putative initiation methione. NR6.1 and NR6.2 are identical to nucleotide 1223 encoding Q407, this represents the end 10 of an exon. NR6.1 splices out an exon present only in NR6.2 and uses a different reading frame for the final exon which is shared with NR6.2. The 3N-untranslated region is shared by NR6.1, NR6.2 and NR6.3, NR6.2 splices in an exon starting with nucleotide 1224 15 encoding D408 and ending with nucleotide 1264 encoding the first nucleotide in the codon for G422 and uses a different reading frame for the final exon which is shared with NR6.2 (see Figure 1). NR6.3 fails to splice from position nucleotide 1224, therefore, translation 20 continues through the intron, giving rise to the C-terminal protein region.

The sequence of NR6 cDNA products generated by 5'-RACE amplification from mouse brain cDNA preparation is 25 shown in SEQ ID NO:18. The nucleotide sequence identified using 5'-RACE appeared to be identical to the sequence of cDNAs encoding NR6.1, NR6.2, and NR6.3 from nucleotide C151, the first nucleotide for the codon for Pro51. 5' of this nucleotide, the sequences diverged 30 and the sequence is unique not being found in NR6.1, NR6.2 or NR6.3. Additionally, there is a single nucleotide difference, with the sequence from the RACE containing an G rather than an A at nucleotide 475, resulting in Thr159 becoming Ala.

35

Analysis of the genomic clones, revealed that they were overlapping and contained exons encoding the majority of

the coding region of the three forms of NR6 (Figures 1, 2 and 3). These genomic clones, contained exons encoding from Asp50 (nucleotide 148) of the NR6 cDNAs. Sequence 5' of this in the cDNAs, including the 5'- untranslated region and the region encoding Met1 to Gln49 (SEQ ID NOs:12, 14 and 16), and the 5' end predicted from analysis of 5' RACE products (SEQ ID NO:18) were not present in the two genomic clones isolated.

10

Analysis of the NR6 genomic DNA clones also provided an explanation of the three classes of NR6 cDNAs found. It is likely that NR6.1, NR6.2 and NR6.3 arise through alternative splicing of NR6 mRNA (Figure 1). The last amino acid residue that these different NR6 proteins are predicted to share is Gln407. SEQ ID NO:18 shows that Gln407 is the last amino acid encoded by the exon that covers nucleotides g5850 to g6037 (see Figure 2). Alternative splicing from the end of this exon (Figure 1) accounts for the generation of cDNAs encoding NR6.1 (SEQ ID NO:12), NR6.2 (SEQ ID NO:14) and NR6.3 (SEQ ID NO:16). In the case of NR6.1, the region from g6038 to g6425 is spliced out, leading to juxtaposition of g6037 and g6426. In the case of NR6.2, the region from g6038 to 6141 is spliced out, an exon from 6142 to g6183 is retained and then this is followed by splicing out of the region from g6183 to g6425. NR6.3 appears to arise when there is no splicing from nucleotide g6038. For all three forms, a secreted rather than transmembrane form is generated, these differ however in their predicted C-terminal region. The genomic NR6 sequence with additional 5N sequence is shown in Figure 3.

EXAMPLE 7

35

ESTs

Databases were searched with the murine NR6

corresponding to the unspliced version shown in SEQ ID NO:16. The murine NR6 sequence used is shown in SEQ ID NO:22.

The databases searched were:

5

(i) dbEST - Database of Expressed Sequence Tags
National Center for Biotechnology Information National
Library of Medicine, 38A, 8N8058600 Rockville Pike,
Bethesda, MD 20894 Phone: 0011-1-301-496-2475 Fax:
10 0015-1-301-480-9241 USA.

(ii) DNA Data Bank of Japan DNA Database Release 3689.
Prepared by: Sanzo Miyazawa Manager/Database
Administrator Hidenori Hayashida Scientific Reviewer
15 Yukiko Yamazaki/Eriko Hatada/Hiroaki Serizawa
Annotators/reviewers Motono Horie/Shigeko Suzuki/Yumiko
Satao Secretaries/typists DNA Data Bank of Japan National
Institute of Genetics Center for Genetic Information
research Laboratory of Genetic Information Analyses 1111
20 Yata Mishima, Shizuoka 411 Japan.

(iii) EMBL Nucleic Acid Sequence Data Bank Release
47.0.

25 (iv) EMBL Nucleic Acid Sequence Data Bank Weekly Updates
Since Release 44.

(v) Genetic Sequence Data Bank NCBI-GenBank Release 94
National Center for Biotechnology Information National
30 Library of Medicine, 38A, 8N805 8600 Rockville Pike,
Bethesda, MD 20894 Phone: 0011-1-301-495-2475 Fax:
0015-1-301-480-9241 USA.

35 (vi) Cumulative Updates since NCBI-GenBank Release 88
National Center for Biotechnology Information National
Library of Medicine, 38A, 8N805 8600 Rockville Pike,
Bethesda, MD 20894 USA.

The search of the databases with the murine probe identified several EST's having sequence similarity to the probe. The EST's were:

- 5 W66776 (murine sequence)
 MM5839 (murine sequence)
 AA014965 (murine sequence)
 W46604 (human sequence)
 W46603 (human sequence)
10 H14009 (human sequence)
 N78873 (human sequence)
 R87407 (human sequence).

EXAMPLE 8

15 Isolation of 3N cDNA clones encoding human NR6

PCR products encoding human NR6 were generated using oligonucleotides UP1 and LP1 (see below) based on human ESTs (Genbank Acc:H14009, Genbank Acc:AA042914) that 20 were identified from databases searched with murine NR6 sequence (SEQ ID NO:22). PCR was performed on a human fetal liver cDNA library (Marathon ready cDNA CLONTECH #7403-1) using Advantage Klen Taq Polymerase mix (CLONTECH #8417-1) in the buffer supplied at 94°C fro 25 30s and 68°C for 3 min for 35 cycles followed by 68°C for 4 min and then stopping at 15°C. A standard PCR programme for the Perkin-Elmer GeneAmp PCT system 2400 thermal cycle was used. The PCR yielded a prominent product of approximately 560 base pairs (bp; SEQ ID NO:18), which was radiolabelled with $[{}^{-32}P]$ dCTP using a 30 random priming method (Amersham, RPN, 1607, Mega prime kit) and used to screen a human fetal kidney 5N-STRETCH PLUS cDNA library (CLONTECH #HL1150x). Library screens were performed using Rapid Hybridisation Buffer 35 (Amersham, RPN 1636) according to manufacturer's instructions and membranes washed at 65°C for 30 min in 0.1xSSC/0.1% (w/v) SDS. Two independent cDNA clones

were obtained as lambda phage and subsequently subcloned and sequenced. Both clones (HFK-63 and HFK-66) contained 1.4 kilobase (kb) inserts that showed sequence similarity with murine NR6. The sequence and 5 corresponding amino acid translation of HFK-66 is shown in SEQ ID NO:24.

The translation protein sequences of clone HFK-66 shows a high degree of sequence similarity with the mouse NR6. 10

OLIGONUCLEOTIDES

UP1: 5NTCC AGG CAG CGG TCG GGG GAC AAC 3N [SEQ ID NO:26]

LP1: 5N TTG CTC ACA TCG TCC ACC ACC TTC 3N [SEQ ID
NO:27]

15

EXAMPLE 9

Genomic Structure of Human NR6

Human genomic DNA clones encoding human NR6 was 20 isolated by screening a human genomic library (Lambda FIXJII Stratagene 946203) with radiolabelled oligonucleotides, 2199 and 2200 (see below). These oligonucleotides were designed based on human ESTs (Genbank Acc:R87407, Genbank Acc:H14009) that were 25 identified from databases searched with murine NR6. Filters were hybridised overnight at 37°C in 6xSSC containing 2 mg/ml bovine serum albumin, 2 mg/ml Ficoll, 2mg/ml polyvinylpyrrolidone, 100 mM ATP, 10 mg/ml tRNA, 2 mM sodium pyrophosphate, 2 mg/ml salmon sperm DNA, 30 0.1% (w/v) SDS and 200 mg/ml sodium azide and washed at 65°C in 6 x SSC/0.1% SDS. Five independent genomic clones were obtained and sequenced. The extend of sequence obtained has determined that the clones overlap and exhibit a similar genomic structure to murine NR6. 35 Exon coding regions are almost identical over the region covered by the genomic clones while intron coding regions differ, although the size of the introns are

comparable. The extent of known overlap is shown in Fig. 5.

OLIGONUCLEOTIDES:

5

2199: 5N CCC ACG CTT CTC ATC GGA TTC TCC CTG 3N [SEQ ID NO:36]

2200: 5N CAG TCC ACA CTG TCC TCC ACT CGG TAG 3N [SEQ ID NO:37]

10

EXAMPLE 10

Northern Blot Analysis of Human NR6 mRNA Expression

15 Clontech Multiple Tissue Northern Blots (Human MTN Blot, CLONTECH #7760-1, Human MTN Blot IV, CLONTECH #7766-I, Human Brain MTN Blot II, CLONTECH #7755-1, Human Brain MTN Blot III, CLONTECH #7750) were probed with a radiolabelled 3N human NR6 cDNA clone, HFK-66 (SEQ ID NO:24). The clone was labelled with $[{}^{-32}P]$ dCTP using a random priming method (Amersham, RPN 1607, Mega prime kit). Hybridisation was performed in Express Hybridisation Solution (CLONTECH H50910) for 3 hours at 67°C and membranes were washed in 0.1xSSC/0.1% w/v SDS at 50°C.

20

25

A 1.8 kb transcript was detected in a variety of human tissues encompassing reproductive, digestive and neural tissues. High levels were observed in the heart, placenta, skeletal muscle, prostate and various areas of the brain, lower levels were observed in the testis, uterus, small intestine and colon. Photographs showing these Northern blots are available upon request. This expression pattern differs from the expression pattern observed with murine NR6.

30

35

EXAMPLE 11

Mouse NR6 Expression Vectors

pEF-FLAG/mNR6.1

5 The mature coding region of mouse NR6.1 was amplified using the PCR to introduce an in-frame *Asc* I restriction enzyme site at the 5' end of the mature coding region and an *Mlu* I site at the 3' end, using the following oligonucleotides:-

10 5N oligo 5N-AGCTGGCGCGCCTCCGGGCGGATCGGGAGCCCAC-3N [SEQ ID NO:30]
3N oligo 5N-AGCTACGCGTTAGAGTTAGCCGGCAG-3N [SEQ ID NO:31]

15 The resulting PCR derived DNA fragment was then digested with *Asc* I and *Mlu* I and cloned into the *Mlu* I site of pEF-FLAG. Expression of NR6 is under the control of the polypeptide chain elongation factor 1 α promoter as described (16) and results in the secretion, using the IL3 signal sequence from pEF-FLAG, of N-terminal FLAG-tagged NR6 protein.

20 25 pEF-FLAG was generated by modifying the expression vector pEF-BOS as follows:-

pEF-BOS (16) was digested with *Xba* I and a linker was synthesized that encoded the mouse IL3 signal sequence (MVLASSTTSIHTMLLLLLMLFHLGLQASIS) and the FLAG epitope (DYKDDDDK). *Asc* I and *Mlu* I restriction enzyme sites were also introduced as cloning sites. The sequence of the linker is as follows:-

30
35 M V L A S S T T S I H T
CTAGACTAGTGCTGACACAATGGTTCTGCCAGCTCTACCACCAGCATCCACACCA
TG

TGATCACGACTGTGTTACCAAGAACGGTCGAGATGGTGGTCGTAGGTGTGGTAC

L L L L M L F H L G L Q A S I S Asc
5 I
CTGCTCCTGCTCCTGATGCTCTTCCACCTGGACTCCAAGCTTCAATCTCGGCGCG
CC
GACGAGGACGAGGACTAGCAGAAGGTGGACCCTGAGGTTCGAAGTTAGAGCCGCGC
GG
10 D Y K D D D D K Mlu I
AGGACTACAAGGACGACGATGACAAGACGCGTGCTAGCACTAGT

TCCTGATGTTCTGCTGCTACTGTTCTGCGCACGATCGTGATCAGATC

15 The two oligonucleotides were annealed together and
ligated into the Xba I site of pEF-BOS to give pEF-FLAG.

pCOS1/FLAG/mNR6 & pCHO1/FLAG/mNR6

20 A DNA fragment containing the sequences encoding IL3
signal sequence/Flag/mNR6 and the poly(A) adenylation
signal from human G-CSF cDNA, was excised from pEF-
FLAG/mNR6 using the restriction enzyme EcoR I. This DNA
25 fragment was then inserted into the EcoR I cloning site
of pCOS1 and pCHO1

The pCOS1 and pCHO1 vectors were constructed as follows.
pCHO1 is also described in reference (17) but with a
30 different selectable marker.

pCOS1 was prepared by digesting HEF-12h-g"1 (see Figure
24 of International Patent Publication No. WO 92/19759)
with EcoRI and SmaI and ligating the digesting product
35 with an EcoRI-NotI-BamHI adaptor (Takara 4510). The
resulting plasmid comprises an EFI" promoter/enhancer,
Nco^r marker gene, SV40E, ori and an Amp^r marker gene.

pCH01 was constructed by digesting DHFR-PMh-gr1 (see Figure 25 of International Patent Publication No. WO 92/19759) with *Pvu*I and *Eco*47III and ligating same with pCOSI digested with *Pvu*I and *Eco*47III. The resulting 5 vector, pCH01, comprises an EFI" promoter/enhancer, an DHFR marker gene, SV40E, Ori and a Amp^r gene.

EXAMPLE 12

10 mRN6 has been expressed as an NN Flag tagged protein following transfection of CHO cells and as a CN Flag tagged protein following transfection of KUSA cells in both cases varying levels of dimeric and aggregated NR6
15 were secreted.

EXAMPLE 13

Murine NR6 expression

20 NR6 expression studies were conducted in murine Northern Blots. At the level of sensitivity used in the adult mouse, NR6 expression was detected in salivary gland, lung and testis. During embryonic development, NR6 is
25 expressed in fetal tissues from day 10 of gestation through to birth. In cell lines, NR6 expression has been observed in the T-lymphoid line CTLL-2 as well as in FD-PyMT (FDC-P1 myeloid cells expressing polyoma middle T gene), and fibroblastoid cells including bone
30 marrow and fetal liver stromal lines.

EXAMPLE 14

Expression, purification and characterisation of CHO and KUSA mNR6

35 The methods provide for the production of a dimeric form of CHO derived NN FLAG-mNR6 without refolding. All

other methods are capable of producing NR6 and are encompassed by the present invention.

5 A. Production of CHO derived N' FLAG-mNR6 (dimeric form)

(i) Protein Production

To analyse structure and functional activity, a cDNA fragment containing the entire coding sequence of murine NR6 with an N-terminal FLAG (NN FLAG) sequence was cloned into the EcoR1 site of the expression vector pCHO1. For stable production of N-terminal FLAG-tagged NR6 the vector contains the DHFR (dihydrofolate reductase) gene as a selective marker with the NR6 gene under the control of an EF1a promoter. CHO cells were transfected with the construct using a polycationic liposome transfection reagent (Lipofectamine, GibcoBRL).

20 (ii) . Lipofectamine transfection method

Using six well tissue culture plates either 2×10^5 KUSA cells in 2ml IMDM + 10% (v/v) FCS or 2×10^5 CHO cells were cultured in 2ml "-MEM + 10% (v/v) FCS until 70% confluent. 2Fg DNA diluted in 100F1 OPTI-MEM I (Gibco BRL, USA) was mixed gently with 12F1 lipofectamine diluted in 100F1 OPTI-MEM I and incubated at room temperature for 30min to allow DNA complex formation. DNA complexes were gently diluted in a total volume of 1ml of OPTI-MEM I and overlaid onto washed KUSA or CHO cell monolayers. A further 1ml IMDM + 20% (v/v) FCS (KUSA cells) or 1ml "-MEM + 20% (v/v) FCS (CHO cells) was added to transfected cells after 5 hours. At 24 hours, the culture medium was replaced with fresh complete growth medium. At 48 hours after transfection, selection was applied. A methotrexate resistant clone secreting comparatively high levels of NR6 was selected and expanded for further analysis.

(iii) Protein expression

CHO cells were grown to confluence in roller bottles in nucleoside free "-MEM + 10% (v/v) FCS. Selection was
5 maintained by using 100 ng/ml Methotrexate in the conditioned media according to manufacturer instructions. Expression was monitored by Biosensor and harvesting found to be optimal at 3 to 4 days.

10 B. Protein Analysis

(i) Biosensor analysis

Expression and purification was monitored by Biosensor analysis (BiaCoreTM, Sweden) where anti FLAG peptide M2 antibody (Kodak Eastman, USA), specific for the FLAG peptide sequence was bound to the sensorchip. Fractions were analysed for binding to the sensor surface (resonance units) and the sample then removed from the surface using 50 mM Diethylamine pH 12.0 prior to analysis of the next fraction. Immobilisation and running conditions of the Biosensor follow the manufacturer's instructions.
15
20

25 (ii) Protein Production

In order to generate and characterise NR6, conditioned media (2 L) produced by CHO cells was harvested after day 3, post confluence. Conditioned media was
30 concentrated using diafiltration with a 10,000 molecular weight cut-off. (Easy flow, Sartorius, Aus). At a volume of 200 ml (i.e. 10 x concentrated) the sample was buffer exchanged into 20 mM Tris, 0.15M NaCl, 0.02% (v/v) Tween 20 pH 7.5 (Buffer A).

35

(iii) Immunoprecipitation and Western Blot analysis of mNR6

Concentrated conditioned media (1ml) was immunoprecipitated with M2 affinity resin (20Fl, Kodak Eastman). To examine the structural characterisation of mNR6 SDS PAGE was performed under reducing and non-reducing conditions. Separation was performed on NOVEX 4-20% (v/v) Tris/glycine gradient gels and protein transferred on PVDF membrane. Western blots were probed with biotinylated M2 antibody (primary, 1:500) and then streptavidin peroxidase (secondary, 1:3000). Samples were visualised by autoradiography using electrochemiluminescence (ECL, Dupont, USA).

By regressive analysis of prestained standards (BIORAD, Aus.) the molecular weight of the monomeric unit was calculated to be 65,000 daltons. Under non-reducing conditions the molecular weight was calculated to be 127,000 indicating that NR6 is a disulphide linked dimer. A tetrameric complex running at approximately 250,000 daltons was also observed. Although a band running at approximately 50,000 daltons was observed, no monomeric NR6 was detected under non-reducing conditions indicating that the majority of NR6 expressed in this system is disulphide linked.

25 (iv) Affinity Chromatography of mNR6

Concentrated conditioned media (200 ml) was applied to M2 affinity resin (5ml) under gravity. To enhance recovery the unbound fraction was reapplied to the column four times prior to extensive washing of the column with 200 volumes of Buffer A. Biosensor analysis indicates that approximately 20% of the M2 binding originally present in the concentrate remains in the unbound fraction. The bound fraction was eluted from the column using an immunodesorbant (50 ml); actisep (Sterogene Labs, USA).

(v) Ion exchange and Desalting of mNR6

In order to buffer exchange mNR6 prior to anion chromatography, 10 ml batches of the eluted fraction (50 ml) were applied to an XK column (400 x 26 mm I.D.) containing G25 sepharose (Pharmacia, Sweden).
5 Chromatography was developed at 4 ml/min using an FPLC (Pharmacia, Sweden) equipped with an online UV280 and conductivity monitor. The mobile phase was 10 mM Tris, 0.1M NaCl, 0.02% v/v Tween, pH 8.0. 10 ml fractions were
10 collected between 12.5 min and 25 min to optimise recovery and removal of salt. Fractions were analysed by Biosensor analysis and pooled according to binding.

15 All pooled active fractions were diluted with an equal volume of 20 mM Tris, 0.02% (v/v) Tween, pH 8.5 (Buffer B) and then loaded onto a Mono Q 5/5 (Pharmacia, Sweden) at a flow rate of 2 ml/min. The column was washed with buffer B. Elution was performed using a linear gradient
20 between buffer B and buffer B containing 0.6M NaCl over 30 min at a flow rate of 1 ml/min. Fractions (1 minute) were collected and analysed on the Biosensor and also by SDS PAGE and Western blot analysis. Fractions 15 to 26 (approximately 0.4M NaCl) appear to contain the majority
25 of mNR6 as indicated by the Biosensor.

C. Production of CHO derived N' FLAG-mNR6 (monomeric form)

30 (i) Protein Production

A cDNA fragment containing the entire coding sequence of murine NR6 with an N-terminal FLAGJ sequence was cloned into the expression vector pCHO1 for production of N-terminal FLAG-tagged protein. This vector contains a neomycin resistance gene with expression of the NR6 gene under the control of an EF1" promoter. This expression
35

construct was transfected into CHO cells using Lipofectamine (Gibco BRL, USA) according to the manufacturer instructions. Transfected cells were cultured in IMDM + 10% (v/v) FCS with resistant cells selected in geneticin (600Fg/ml, Gibco BRL, USA). A neomycin resistant clone, secreting comparatively high levels of NR6 was selected and expanded for further analysis.

10 (ii) Protein expression

N' FLAG-NR6 expressed in serum free conditioned media (10 litre) was harvested from transfected CHO and cells. Collected media was concentrated using a CH2 ultrafiltration system equipped with a S1Y10 cartridge (Amicon molecular weight cut-off 10,000). Preliminary examination of the expressed product under reducing and non-reducing SDS PAGE followed by western blot analysis was performed. Visualisation of the protein on Westerns was specific to the primary antibody anti FLAG M2. Under reducing conditions a band approximately at 65,000 daltons was observed. Under non-reducing conditions, dimer and larger molecular weight aggregates were observed. These are disulphide linked monomers as they are not present in the reducing gel. Small amounts of monomer appear to be present in non-reducing gels.

25 (iii) Affinity Chromatography of NR6

Concentrated conditioned media was applied to an anti FLAG M2 affinity resin (100 x 16 mm I.D.). After washing the unbound proteins off the column, the bound proteins were eluted using FLAG peptide (60Fg/ml) in PBS.

30 (iv) Ion Exchange Chromatography of NR6

35 Eluted fractions from affinity column were dialysed overnight against 20 mM Tris-HCl pH 8.5 (buffer C)

containing 50 mM Dithiothreitol (DTT) using 25,000 cut-off dialysis tubing (Spectra/Por7, Spectrum). The dialysed fractions were loaded onto Mono Q 5/5 (Pharmacia, Sweden) previously equilibrated with buffer C containing 5 mM DTT. Chromatography was developed using a linear gradient between buffer C and buffer C containing 1.0 M NaCl at a flow rate of 0.5 ml / min.

10 (v) Refolding of NR6

Fractions containing NR6 from the Mono Q were adjusted to 50 mM DTT and left overnight at 41C. To initiated refolding the sample was then dialysed against 50 mM Tris-HCl (pH 8.5), 2 M Urea, 0.1% (v/v) Tween 20, 10 mM Glutathione (reduced) and 2 mM Glutathione (oxidised) at a final protein concentration of 100 Fg / ml. Folding was carried out at ambient temperature with one change of the buffer over 24 hours.

20 (v) Reversed Phase High Performance Liquid Chromatography (RP-HPLC)

The folded product was further purified by RP-HPLC using a Vydac C4 resin (250 x 4.6 mm I.D.) previously equilibrated with 0.1% (v/v) Trifluoroacetic acid (TFA). Elution was carried out using a linear gradient from 0 to 80% (v/v) acetonitrile / 0.1% (v/v) TFA at a flow rate of 1 ml per minute.

30 D. pCHO1/NR6/FLAG

In order to determine the native N termini of NR6, a C terminal FLAG NR6 CHO cell line was established.

35 The plasmid pKUSA166 (murine NR6 cDNA cloned into the EcoR I site of pBLUESCRIPT) was digested with BamH I to remove the sequences encoding the last 15 amino acids of murine NR6. Synthetic oligonucleotides which encode the

3' end of mouse NR6 followed by the FLAG peptide tag were annealed and ligated into the BamH I site of pKUSA166. The sequence of the oligonucleotides was as follows:-

5

I L P S G R R G A A R G P A G D Y K D
D D D K * [SEQ ID NO:34]
GATCTGCCCTGGGCAGACGGGGTGCAGCGAGAGGTCCCTGCCGGCGACTACAAGG
10 ACGACGATGACAAGTA G [SEQ ID NO:33]
AACGGGAGCCCGTCTGCCCAACGCCGCTCTCCAGGACGGCGCTGATGTTCCGTGCT
GCTACTGTTCATCCTAG [SEQ ID NO:35]

The 5' end of the linker introduces a silent mutation (CTG > TTG), to destroy the 5' BamH I site upon insertion of the linker. The NR6 cDNA (with native signal sequence) with the C-terminal FLAG was cut out of pKUSA166 with EcoR I and BamH I and cloned into the EcoR I - BamH I cloning sites of pCHO-1. This vector results in the secretion of NR6 protein with a C-terminal flag tag (CN FLAG-mRN6).

This vector results in the secretion of NR6 protein from KUSA cells. The vector pCHO1 has been previously described in (17) although with a different secretable marker.

(i) Production of polyclonal NR6 antiserum

30 The following peptide from the N terminal area of NR6 was chosen for production of polyclonal antiserum to NR6

VISPQDPPTLLIGSSLQATCSIHGDTP [SEQ ID NO:39]

35 The peptide was conjugated to KLH and injected into rabbits. Production and purification of the polyclonal antibody specific to the NR6 peptide sequence follows

standard methods.

(ii) Protein expression

5 KUSA cells transfected with cDNA of C terminal tagged mNR6 were grown to confluence in flasks (800ml) using IMDM media containing 10% (v/v) FBS. Conditioned media (100 ml) was harvested 3 -4 days post confluence.

10 (iii) Characterisation of NR6 by Immunoprecipitation and Western blotting

In order to establish that NR6 with the predicted sequence is produced in KUSA cells transfected with the 15 cDNA, western blot analysis using both M2 antibody and purified NR6 specific rabbit antibody were performed. Conditioned media (1 to 5 ml) was immunoprecipitated with M2 affinity resin (10-20 Fl). Then after sufficient time for binding, the beads were washed with MT-PBS and 20 subsequently NR6 eluted with 100 Fg/ml FLAG peptide (40 Fl, (1, 5 minute incubation)). The sample was then subjected to reducing and non reducing SDS PAGE followed 25 by western blot analysis. Both purified NR6 polyclonal antibody (purified by protein G) and M2 antibody recognise a band under reducing conditions of a molecular weight size approximately 65,000 daltons. Since the two antibodies reconising resides at the N terminus and C terminus it is reasonable to assume that full length NR6 is produced. Biotinylation of the 30 respective antibodies by standard methods reduces the background. Under non-reducing conditions polyclonal NR6 bind antibodies to a band of a molecular weight of approximately 127,000, consistent with a dimeric NR6 disulphide linked form. Minor components of tetrameric 35 NR6 are present, no monomeric NR6 is evident using polyclonal NR6 antibodies.

EXAMPLE 15
Generation of NR6 knockout mice

To construct the NR6 targeting vector, 4.1kb of genomic
5 NR6 DNA containing exons 2 through to 6 was deleted and
replaced with G418-resistance cassette, leaving 5N and
3N NR6 arms of 2.9 and 4.5 kb respectively. A 4.5 kb
Xhol fragment of the murine genomic NR6 clone 2.2
(Figure 3) containing exons 7, 8 and 3N flanking
10 sequence was subcloned into the XhoI site of pBluescript
generating pBSNR6Xho4.5. A 2.9kb NotI-StuI fragment
within NR6 intron 1 from the same genomic clone was
inserted into NotI and EcoRV digested pBSNR6Xho4.5
creating pNR6-Ex2-6. This plasmid was digested with
15 ClaI, which was situated between the two NR6 fragments,
and following blunt ending, ligated with a blunted 6kb
HindIII fragment from placZneo, which contains the
lacZgene and a PGKneo cassette, to generate the final
targeting vector, pNR6lacZneo. pNR6lacZneo was
20 linearised with NotI and electroporated into W9.5
embryonic stem cells. After 48 hours, transfected cells
were selected in 175 Fg/ml G418 and resistant clones
picked and expanded after a further 8 days.

25 Clones in which the targetting vector had recombined
with the endogenous NR6 gene were identified by
hybridising SpeI-digested genomic DNA with a 0.6 kb
XhoI-StuI fragment from genomic NR6 clone 2.2. This
probe (probe A, Figure 4), which is located 3N to the
30 NR6 sequences in the targeting vector, distinguished
between the endogenous (9.9 kb) and targeted (7.1 kb)
NR6 loci (Figure 5).

Genomic DNA was digested with SpeI for 16hrs at 371C,
35 electrophoresed through 0.8% (w/v) agarose, transferred
to nylon membranes and hybridised to ³²P-labelled probe
in a solution containing 0.5M sodium phosphate, 7% (w/v)

SDS, 1mM EDTA and washed in a solution containing 40mM sodium phosphate, 1% (w/v) SDS at 65°C. Hybridising bands were visualised by autoradiography for 16 hours at -70°C using Kodak XAR-5 film and intensifying screens.

5 Two targeted ES cell clones, W9.5NR6-2-44 and W9.5NR6-4-2, were injected into C57Bl/6 blastocysts to generate chimeric mice. Male chimeras were mated with C57Bl/6 females to yield NR6 heterozygotes which were subsequently interbred to produce wild-type (NR6^{+/+}),

10 heterozygous (NR6⁺⁻) and mutant (NR6^{-/-}) mice. The genotypes of offspring were determined by Southern Blot analysis of genomic DNA extracted from tail biopsies.

15 Genotyping of mice at weaning from matings between NR⁺⁻ heterozygous mice derived from both targated ES cell clones revealed an absence of homozygous NR6^{-/-} mutants. As no unusual loss of mice was observed between birth and weaning, this suggest that lack of NR6 is lethal during embryonic development or immediately after birth.

20 Genotyping of embryonic tissues at various stages of development suggests that death occurs late in gestation (beyond day 16) or at birth.

EXAMPLE 16

25 **Oligonucleotides**

1943:
5' GTC CAA GTG CGT TGT AAC CCA 3'

2070:
5' GCT GAG TGT GCG CTG GGT CTC ACC 3'

30 2057:
5' GGC TCC ACT CGC TCC AGA 3'

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications. The

invention also includes all of the steps, features,
compositions and compounds referred to or indicated in
this specification, individually or collectively, and
any and all combinations of any two or more of said
5 steps or features.

BIBLIOGRAPHY:

1. Du, X.X. and Williams, D.A. (1994) *Blood* 83: 2023-2030.
- 5 2. Yang, Y.C. and Yin, T. (1992) *Biofactors* 4: 15-21.
3. Paul, S.R., Bennett, F., Calvetti, J.A., Kelleher, K., Wood, C.R., O'Hara, R.J.J., Leary, A.C., Sibley, B., Clark, S.C., Williams, D.A. and Yang, Y.-C. (1990) *Proc. Natl. Acad. Sci. USA* 87: 7512.
- 10 4. Musashi, M., Clark, S.C., Sudo, T., Urdal, D.L., and Ogawa, M. (1991) *Blood* 78: 1448-1451.
5. Schibler, K.R., Yang, Y.C. and Christensen, R.D. (1992) *Blood* 80: 900-3.
- 15 6. Tsuji, K., Lyman, S.D., Sudo, T., Clark, S.C., and Ogawa, M. (1992) *Blood* 79: 2855-60.
7. Burstein, S.A., Mei, R.L., Henthorn, J., Friese, P. and turner, K. (1992) *J. Cell. Physiol.* 153: 305-12.
- 20 8. Hangoc, G., Yin, T., Cooper, S., Schendel, P., Yang, Y.C. and Broxmeyer, H.E. (1993) *Blood* 81: 965-72.
9. Teramura, M., Kobayashi, S., Hoshino, S., Oshimi, K. and Mizoguchi, H. (1992) *Blood* 79: 327-31.
- 25 10. Yonemura, Y., Kawakita, M., Masuda, T., Fujimoto, K., Kato, K. and Takatsuki, K. (1992) *Exp. Hematol.* 20: 1011-6.
11. Baumann, H. and Schendel, P. (1991) *J. Biol. Chem.* 266: 20424-7.
- 30 12. Kawashima, I., Ohsumi, J., Mita-Honjo, K., Shimoda-Takano, K., Ishikawa, H., Sakakibara, S., Miyadai, K. and Takiguchi, Y. (1991) *Febs. Lett.* 283: 199-202.
13. Keller, D.C., Du, X.X., Srour, E.f., Hoffman, R. and Williams, D.A. (1993) *Blood* 82: 1428-35.
- 35 14. Sambrook et al (1989) Cloning: A Laboratory Manual. Cold Spring Harbour Laboratory, Cold Spring

- Harbour, NY.
15. Chirgwin et al (1979) *Biochemistry* 18: 5294-5299.
16. Mizushima and Nagata (1990) *Nucl. Acids Res.*, 18:
5322.
- 5 17. *FEBS Lett* (1994) 356: 244-248.
18. Bazan, J.F. (1990) *Proc Natl Acad Sci USA*, 87,
6934-8
- 10 19. de Vos, A.M., Ultsch, M. and Kossiakoff, A.A.
(1992) *Science*, 255, 306-12
- 15 20. Layton, M.J., Cross, B.A., Metcalf, D., Ward, L.D.,
Simpson, R.J. and Nicola, N.A. (1992) *Proceedings
of the National Academy of Sciences of the United
States of America* 89: 8616-8620
- 20 21. Taga, T., Hibi, M., Hirata, T., Tamasaki, K.,
Tasukawa, K., Matsuda, T., Hirano, T. and
Kishimoto, T. (1989) *Cell* 58: 573-581
- 25 22. Merberg, D.M., Wolf, S.F. and Clark, S.C. (1992)
Sequence similarity between NKSF and the IL-6/G-CSF
family (1992) *Immunology Today* 13: 77-78
23. Cearing, D.P. and Cosman, D. (1991) *Cell* 66:9-10
- 30 24. Wrighton, N.C., Farrell, F.X., Chang, R., Kashyap,
A.K., Barbone, F.P., Mulcahy, L.S., Johnson, D.L.,
Barrett, R.W., Jolliffe, L.K. and Dower, W.J.
(1996) *Science* 273: 458-464.
- 35 25. Cwirla, S.E., Balasubramanian, P., Duffin, D.J.,
Wagstrom, C.R., Gates, C.M., Singer, S.C., Davis,
A.M., Tansik, R.L., Mattheakis, L.C., Boytos, C.M.,
Schatz, P.J., Baccanari, D.P., Wrighton, N.C.,
Barret, R.W. and Dower, W.J. (1997) *Science* 276:

1696--9, 1997

26. Samuel Davis et al (1996) *Cell* 87:1161-1169.
- 5 27. Chitra Suri et al (1996) *Cell* 87: 1171-1180.
28. Nicholas C. Wrighton et al (1996) *Science* 273: 458-463.
- 10 29. Oded Livnah et al (1996) *Science* 273: 464-471.
30. Cwirla, Steven E. et al (1997) *Science* 276: 1696-1699.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: (Other than US) AMRAD OPERATIONS PTY LTD

(US only) Douglas James HILTON, Nicos Antony NICOLA, Alison FARLEY, Tracey WILLSON, Jian-Guo ZHANG, Warren ALEXANDER, Steven RAKAR, Louis FABRI, Tetsuo KOJIMA, Masatsugu MAEDA, Yasumfumi KIKUCHI, Andrew NASH

(ii) TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME

15

(iii) NUMBER OF SEQUENCES: 39

(iv) CORRESPONDENCE ADDRESS:

20

(A) ADDRESSEE: DAVIES COLLISON CAVE
(B) STREET: 1 LITTLE COLLINS STREET
(C) CITY: MELBOURNE
(D) STATE: VICTORIA
(E) COUNTRY: AUSTRALIA
25 (F) ZIP: 3000

(v) COMPUTER READABLE FORM:

30

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version

#1.25

(vi) CURRENT APPLICATION DATA:

35

(A) APPLICATION NUMBER:

PCT INTERNATIONAL APPLICATION

(B) FILING DATE: 11-SEP-1997

5 (vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PO2246/96
(B) FILING DATE: 11-SEP-1996

10 (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: HUGHES DR, E JOHN L
(C) REFERENCE/DOCKET NUMBER: EJH/AF

15 (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: +61 3 9254 2777
(B) TELEFAX: +61 3 9254 2770

20 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp Ser Xaa Trp Ser

30 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5

ACTCGCTCCA GATTCCCGCC TTTT

24

10 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

25 TCCCCGCCTTT TTTCGACCCAT AGAT

24

(2) INFORMATION FOR SEQ ID NO:4:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGTACTTGGC TTGGAAGAGG AAAT

24

(2) INFORMATION FOR SEQ ID NO:5:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGCTCACGT GCACGTCGGG TGGG

24

(2) INFORMATION FOR SEQ ID NO:6:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCTGCTGTT AAAGGGCTTC TC

22

35

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: Oligonucleotide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

15 (A/G) CTCCA (A/G) TC (A/G) CTCCA

15

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: Oligonucleotide

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

30 (A/G) CTCCA (C/T) TC (A/G) CTCCA

15

(2) INFORMATION FOR SEQ ID NO:9:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

10

AAGTGTGACC ATCATGTGGA C

21

15 (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

30 GGAGGTGTTA AGGAGGCG

18

(2) INFORMATION FOR SEQ ID NO:11:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

10

ATGCCCGCGG GTCGCCCG

18

15 (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

30

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1242

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCACGAGCT TCGCTGTCCG CGCCCAGTGA CGCGCGTGCG GACCCGAGCC CCAATCTGCA	-64
35 CCCCGCAGAC TCGCCCCCGC CCCATAACCGG CGTTGCAGTC ACCGCCCGTT GCGCGCCACC	-4
CCC	-3
ATG CCC GCG GGT CGC CCG GGC CCC GTC GCC CAA TCC GCG CGG CGG CCG	48

	Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro		
1	5	10	15
5	CCG CGG CCG CTG TCC TCG CTG TGG CCT CTG TTG CTC TGT GTC CTC		96
	Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu		
	20	25	30
10	GGG GTG CCT CGG GGC GGA TCG GGA GCC CAC ACA GCT GTA ATC AGC CCC		144
	Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro		
	35	40	45
15	CAG GAC CCC ACC CTT CTC ATC GGC TCC TCC CTG CAA GCT ACC TGC TCT		192
	Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser		
	50	55	60
20	ATA CAT GGA GAC ACA CCT GGG GCC ACC GCT GAG GGG CTC TAC TGG ACC		240
	Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr		
	65	70	75
25	CTC AAT GGT CGC CGC CTG CCC TCT GAG CTG TCC CGC CTC CTT AAC ACC		288
	Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr		
	85	90	95
30	TCC ACC CTG GCC CTG GCC CTG GCT AAC CTT AAT GGG TCC AGG CAG CAG		336
	Ser Thr Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln		
	100	105	110
35	TCA GGA GAC AAT CTG GTG TGT CAC GCC CGA GAC GGC AGC ATT CTG GCT		384
	Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala		
	115	120	125
	GGC TCC TGC CTC TAT GTT GGC TTG CCC CCT GAG AAG CCC TTT AAC ATC		432
	Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile		
	130	135	140

	AGC TGC TGG TCC CGG AAC ATG AAG GAT CTC ACG TGC CGC TGG ACA CCG	480
	Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro	
145	150	155
		160
5	GGT GCA CAC GGG GAG ACA TTC TTA CAT ACC AAC TAC TCC CTC AAG TAC	528
	Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr	
	165	170
		175
10	AAG CTG AGG TGG TAC GGT CAG GAT AAC ACA TGT GAG GAG TAC CAC ACT	576
	Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr	
	180	185
		190
15	GTG GGC CCT CAC TCA TGC CAT ATC CCC AAG GAC CTG GCC CTC TTC ACT	624
	Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr	
	195	200
		205
20	CCC TAT GAG ATC TGG GTG GAA GCC ACC AAT CGC CTA GGC TCA GCA AGA	672
	Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg	
	210	215
		220
	TCT GAT GTC CTC ACA CTG GAT GTC CTG GAC GTG GTG ACC ACG GAC CCC	720
	Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro	
	225	230
		235
		240
25	CCA CCC GAC GTG CAC GTG AGC CGC GTT GGG GGC CTG GAG GAC CAG CTG	768
	Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu	
	245	250
		255
30	AGT GTG CGC TGG GTC TCA CCA CCA GCT CTC AAG GAT TTC CTC TTC CAA	816
	Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln	
	260	265
		270
35	GCC AAG TAC CAG ATC CGC TAC CGC GTG GAG GAC AGC GTG GAC TGG AAG	864
	Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys	
	275	280
		285

	GTG GTG GAT GAC GTC AGC AAC CAG ACC TCC TGC CGT CTC GCG GGC CTG	912		
	Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu			
	290	295	300	
5	AAG CCC GGC ACC GTT TAC TTC GTC CAA GTG CGT TGT AAC CCA TTC GGG	960		
	Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly			
	305	310	315	320
10	ATC TAT GGG TCG AAA AAG GCG GGA ATC TGG AGC GAG TGG AGC CAC CCC	1008		
	Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro			
	325	330	335	
15	ACC GCT GCC TCC ACC CCT CGA AGT GAG CGC CCG GGC CCG GGC GGG	1056		
	Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly			
	340	345	350	
20	GTG TGC GAG CCG CGG GGC GAG CCC AGC TCG GGC CCG GTG CGG CGC	1104		
	Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg			
	355	360	365	
	GAG CTC AAG CAG TTC CTC GGC TGG CTC AAG AAG CAC GCA TAC TGC TCG	1152		
	Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser			
	370	375	380	
25	AAC CTT AGT TTC CGC CTG TAC GAC CAG TGG CGT GCT TGG ATG CAG AAG	1200		
	Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys			
	385	390	395	400
30	TCA CAC AAG ACC CGA AAC CAG GTC CTG CCG GCT AAA CTC TAAGGATAGG	1249		
	Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu			
	405	410		
	CCATCCTCCT GCTGGGTCA G ACCTGGAGGC TCACCTGAAT TGGAGCCCC CTGTACCATC	1309		
35	TGGGCAACAA AGAACCTAC CAGAGGCTGG GGCACAATGA GCTCCCACAA CCACAGCTT	1369		
	GGTCCACATG ATGGTCACAC TTGGATATAAC CCCAGTGTGG GTAAGGTTGG GGTATTGCAG	1429		

GGCCTCCCAA CAATCTCTTT AAATAAATAA AGGAGTTGTT CAGGTAAAAA AAAAAAAAAA 1489
AAAAAAAAAA AAAAAAAA 1506

5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 413 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro
1 5 10 15

20 Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
20 25 30

Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
35 40 45

25 Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
50 55 60

Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
30 65 70 75 80

Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
85 90 95

35 Ser Thr Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln
100 105 110

Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala
115 120 125

Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile
5 130 135 140

Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro
145 150 155 160

10 Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr
165 170 175

Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr
180 185 190

15 Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr
195 200 205

Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg
20 210 215 220

Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
225 230 235 240

25 Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
245 250 255

Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
260 265 270

30 Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
275 280 285

Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
35 290 295 300

Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
305 310 315 320

Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
5 325 330 335

Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
340 345 350

10 Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
355 360 365

Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
370 375 380

15 Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
385 390 395 400

Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu
20 405 410

(2) INFORMATION FOR SEQ ID NO:14:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCACGAGCT TCGCTGTCCG CGCCCAGTGA CGCGCGTGCG GACCCGAGCC CCAATCTGCA -65
 5 CCCCGCAGAC TCGCCCCCGC CCCATACCGG CGTTGCAGTC ACCGCCCGTT GCGCGCCACC -5
 CCCA -1
 10 ATG CCC GCG GGT CGC CCG GGC CCC GTC GCC CAA TCC GCG CGG CGG CCG 48
 Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro
 1 5 10 15
 15 CCG CGG CCG CTG TCC TCG CTG TGG TCG CCT CTG TTG CTC TGT GTC CTC 96
 Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
 20 25 30
 20 GGG GTG CCT CGG GGC GGA TCG GGA GCC CAC ACA GCT GTA ATC AGC CCC 144
 Gly Val Pro Arg Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
 25 35 40 45
 25 CAG GAC CCC ACC CTT CTC ATC GGC TCC TCC CTG CAA GCT ACC TGC TCT 192
 Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
 30 50 55 60
 30 ATA CAT GGA GAC ACA CCT GGG GCC ACC GCT GAG GGG CTC TAC TGG ACC 240
 Ile His Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
 65 70 75 80
 35 CTC AAT GGT CGC CGC CTG CCC TCT GAG CTG TCC CGC CTC CTT AAC ACC 288
 Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
 85 90 95
 35 TCC ACC CTG GCC CTG GCC CTG GCT AAC CTT AAT GGG TCC AGG CAG CAG 336
 Ser Thr Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln
 100 105 110

	TCA GGA GAC AAT CTG GTG TGT CAC GCC CGA GAC GGC AGC ATT CTG GCT		384
	Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala		
	115	120	125
5	GGC TCC TGC CTC TAT GTT GGC TTG CCC CCT GAG AAG CCC TTT AAC ATC		432
	Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile		
	130	135	140
10	AGC TGC TGG TCC CGG AAC ATG AAG GAT CTC ACG TGC CGC TGG ACA CCG		480
	Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro		
	145	150	155
	160		
15	GGT GCA CAC GGG GAG ACA TTC TTA CAT ACC AAC TAC TCC CTC AAG TAC		528
	Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr		
	165	170	175
20	AAG CTG AGG TGG TAC GGT CAG GAT AAC ACA TGT GAG GAG TAC CAC ACT		576
	Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr		
	180	185	190
25	GTG GGC CCT CAC TCA TGC CAT ATC CCC AAG GAC CTG GCC CTC TTC ACT		624
	Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr		
	195	200	205
30	CCC TAT GAG ATC TGG GTG GAA GCC ACC AAT CGC CTA GGC TCA GCA AGA		672
	Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg		
	210	215	220
35	TCT GAT GTC CTC ACA CTG GAT GTC CTG GAC GTG GTG ACC ACG GAC CCC		720
	Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro		
	225	230	235
	240		
40	CCA CCC GAC GTG CAC GTG AGC CGC GTT GGG GGC CTG GAG GAC CAG CTG		768
	Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu		
	245	250	255

	AGT GTG CGC TGG GTC TCA CCA CCA GCT CTC AAG GAT TTC CTC TTC CAA	816		
	Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln			
	260	265	270	
5	GCC AAG TAC CAG ATC CGC TAC CGC GTG GAG GAC AGC GTG GAC TGG AAG	864		
	Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys			
	275	280	285	
10	GTG GTG GAT GAC GTC AGC AAC CAG ACC TCC TGC CGT CTC GCG GGC CTG	912		
	Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu			
	290	295	300	
15	AAG CCC GGC ACC GTT TAC TTC GTC CAA GTG CGT TGT AAC CCA TTC GGG	960		
	Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly			
	305	310	315	320
20	ATC TAT GGG TCG AAA AAG GCG GGA ATC TGG AGC GAG TGG AGC CAC CCC	1008		
	Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro			
	325	330	335	
	ACC GCT GCC TCC ACC CCT CGA AGT GAG CGC CCG GGC CCG GGC GGG	1056		
	Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly			
	340	345	350	
25	GTG TGC GAG CCG CGG GGC GGC GAG CCC AGC TCG GGC CCG GTG CGG CGC	1104		
	Val Cys Glu Pro Arg Gly Glu Pro Ser Ser Gly Pro Val Arg Arg			
	355	360	365	
30	GAG CTC AAG CAG TTC CTC GGC TGG CTC AAG AAG CAC GCA TAC TGC TCG	1152		
	Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser			
	370	375	380	
35	AAC CTT AGT TTC CGC CTG TAC GAC CAG TGG CGT GCT TGG ATG CAG AAG	1200		
	Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys			
	385	390	395	400

	TCA CAC AAG ACC CGA AAC CAG GAC GAG GGG ATC CTG CCT TCG GGC AGA	1248
	Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly Arg	
	405	410
		415
5	CGG GGT GCG GCG AGA GGT CCT GCC GGT TAAACTCTAA GGATAGGCCA	1295
	Arg Gly Ala Ala Arg Gly Pro Ala Gly	
	420	425
10	TCCTCCTGCT GGGTCAGACC TGGAGGCTCA CCTGAATTGG AGCCCTCTG TACCATCTGG	1355
	GCAACAAAGA AACCTACCAG AGGCTGGGC ACAATGAGCT CCCACAACCA CAGCTTTGGT	1415
	CCACATGATG GTCACACTTG GATATACCCC AGTGTGGTA AGGTTGGGT ATTGCAGGGC	1475
15	CTCCCAACAA TCTCTTAAA TAAATAAAGG AGTTGTTCA GTAAAAAAAAA AAAAAAAA	1535
	AAAAAAA AAAA	1549

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- 25 (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro			
1	5	10	15
35 Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu			
20	25	30	

Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
35 40 45

Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
5 50 55 60

Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
65 70 75 80

10 Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
85 90 95

Ser Thr Leu Ala Leu Ala Leu Asn Leu Asn Gly Ser Arg Gln Gln
100 105 110

15 Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala
115 120 125

Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile
20 130 135 140

Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro
145 150 155 160

25 Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr
165 170 175

Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr
180 185 190

30 Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr
195 200 205

Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg
35 210 215 220

Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
225 230 235 240

Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
5 245 250 255

Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
260 265 270

10 Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
275 280 285

Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
290 295 300

15 Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
305 310 315 320

Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
20 325 330 335

Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
340 345 350

25 Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
355 360 365

Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
370 375 380

30 Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
385 390 395 400

Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly Arg
35 405 410 415

Arg Gly Ala Ala Arg Gly Pro Ala Gly

420

425

5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 938 base pairs
- 10 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..468

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

25	GGC ACC GTT TAC TTC GTC CAA GTG CGT TGT AAC CCA TTC GGG ATC TAT	48
	Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr	
	1 5 10 15	
	GGG TCG AAA AAG GCG GGA ATC TGG AGC GAG TGG AGC CAC CCC ACC GCT	96
30	Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala	
20	25 30	
	GCC TCC ACC CCT CGA AGT GAG CGC CCG GGC CCG GGC GGC GGG GTG TGC	144
	Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Val Cys	
35	35 40 45	

	GAG CCG CGG GGC GGC GAG CCC AGC TCG GGC CCG GTG CGG CGC GAG CTC	192		
	Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu			
	50	55	60	
5	AAG CAG TTC CTC GGC TGG CTC AAG AAG CAC GCA TAC TGC TCG AAC CTT	240		
	Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu			
	65	70	75	80
10	AGT TTC CGC CTG TAC GAC CAG TGG CGT GCT TGG ATG CAG AAG TCA CAC	288		
	Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His			
	85	90	95	
15	AAG ACC CGA AAC CAG GTA GGA AAG TTG GGG GAG GCT TGC GTG GGG GGT	336		
	Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly			
	100	105	110	
20	AAA GGA GCA GAG GAA GAG AGA GAC CCG GGT GAG CAG CCT CCA CAA CAC	384		
	Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His			
	115	120	125	
	CGC ACT CTT CTT TCC AAG CAC AGG ACG AGG GGA TCC TGC CCT CGG GCA	432		
	Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala			
	130	135	140	
25	GAC GGG GTG CGG CGA GAG GTA AGG GGG TCT GGG TGAGTGGGGC CTACAGCAGT	485		
	Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly			
	145	150	155	
30	CTAGATGAGG CCCTTTCCCC TCCTTCGGTG TTGCTCAAAG GGATCTCTTA GTGCTCATTT	545		
	CACCCACTGC AAAGAGCCCC AGGTTTTACT GCATCATCAA GTTGCTGAAG GGTCCAGGCT	605		
	TAATGTGGCC TCTTTCTGC CCTCAGGTCC TGCCGGCTAA ACTCTAAGGA TAGGCCATCC	665		
35	TCCTGCTGGG TCAGACCTGG AGGCTCACCT GAATTGGAGC CCCTCTGTAC CTATCTGGGC	725		
	AACAAAGAAA CCTACCATGA GGCTGGGGCA CAATGAGCTC CCACAACCAC AGCTTTGGTC	785		

CACATGATGG TCACACTTGG ATATACCCCA GTGTGGGTAA GGTTGGGTAA TTGCAGGGCC 845
TCCCAACAAT CTCTTTAAAT AAATAAAGGA GTTGTCAGG TAAAAAAA AAAAAAAA 905
5 AAAAAAAA AAAAAAAA AAAAAAAA AAA 938

(2) INFORMATION FOR SEQ ID NO:17:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
20 1 5 10 15
Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala
20 25 30
25 Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Val Cys
35 40 45
Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu
50 55 60
30 Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu
65 70 75 80
Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His
35 85 90 95

Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly
100 105 110

Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His
5 115 120 125

Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala
130 135 140

10 Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly
145 150 155

15 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..834

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCC ACC CTT CTC ATC GGC TCC TCC CTG CAA GCT ACC TGC TCT ATA CAT 98
Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His
35 51 55 60 65

	GGA GAC ACA CCT GGG GCC ACC GCT GAG GGG CTC TAC TGG ACC CTC AAT	146	
	Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn		
	70	75	80
5	GGT CGC CGC CTG CCC TCT GAG CTG TCC CGC CTC CTT AAC ACC TCC ACC	194	
	Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr		
	85	90	95
10	CTG GCC CTG GCC CTG GCT AAC CTT AAT GGG TCC AGG CAG CAG TCA GGA	242	
	Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser Gly		
	100	105	110
15	GAC AAT CTG GTG TGT CAC GCC CGA GAC GGC AGC ATT CTG GCT GGC TCC	290	
	Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser		
	115	120	125
	TGC CTC TAT GTT GGC TTG CCC CCT GAG AAG CCC TTT AAC ATC AGC TGC	338	
	Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser Cys		
	135	140	145
20	TGG TCC CGG AAC ATG AAG GAT CTC ACG TGC CGC TGG ACA CCG GGT GCA	386	
	Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala		
	150	155	200
25	CAC GGG GAG ACA TTC TTA CAT ACC AAC TAC TCC CTC AAG TAC AAG CTG	434	
	His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu		
	205	210	215
30	AGG TGG TAC GGT CAG GAT AAC ACA TGT GAG GAG TAC CAC ACT GTG GGG	482	
	Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly		
	220	225	230
35	CCC CAC TCA TGC CAT ATC CCC AAG GAC CTG GCC CTC TTC ACT CCC TAT	530	
	Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr		
	235	240	245
		250	

	GAG ATC TGG GTG GAA GCC ACC AAT CGC CTA GGC TCA GCA AGA TCT GAT	578
	Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp	
	255	260
	265	
5	GTC CTC ACA CTG GAT GTC CTG GAC GTG GTG ACC ACG GAC CCC CCA CCC	626
	Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro Pro Pro	
	270	275
	280	
10	GAC GTG CAC GTG AGC CGC GTT GGG GGC CTG GAG GAC CAG CTG AGT GTG	674
	Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val	
	285	290
	295	
15	CGC TGG GTC TCA CCA CCA GCT CTC AAG GAT TTC CTC TTC CAA GCC AAG	722
	Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys	
	300	305
	310	
20	TAC CAG ATC CGC TAC CGC GTG GAG GAC AGC GTG GAC TGG AAG GTG GTG	770
	Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val	
	315	320
	325	330
25	GAT GAC GTC AGC AAC CAG ACC TCC TGC CGT CTC GCG GGC CTG AAG CCC	818
	Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro	
	335	340
	345	
30	GGC ACC GTT TAC TTC GTC CAA GTG CGT TGT AAC CCA TTC GGG ATC TAT	866
	Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr	
	350	355
	360	
	GGG TCG AAA AAG GCG GGA	894
35	Gly Ser Lys Lys Ala Gly	
	365	

(2) INFORMATION FOR SEQ ID NO:19:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His
10 51 55 60 65

Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn
70 75 80

15 Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr
 85 90 95

Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser Gly
100 105 110

20 Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser
 115 120 125 130

Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser Cys
25 135 140 145

Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala
150 155 200

30 His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu
 205 210 215

Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly
220 225 230

35 Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr
 235 240 245 250

Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp
255 260 265

Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro Pro Pro
5 270 275 280

Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val
285 290 295

10 Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys
300 305 310

Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val
315 320 325 330

15 Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro
335 340 345

Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
20 350 355 360

Gly Ser Lys Lys Ala Gly
365

25 (2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 143 base pairs
(B) TYPE: nucleic acids
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCATGAAGG CTTAGGGTGG GGATCGGTAG GACCCATGCA CCCAGAGAAA GGGACTGGTG 60
GCAACTTTCA AACTCTCTGG GGAAGGAAGA AGGGCTGAAA GAGG 104
5 ATG AAC GGG CTC AGA CAC AGC TGT AAT CAG CCC CCA GGA 143
Met Asn Gly Leu Arg His Ser Cys Asn Gln Pro Pro Gly
5 10

10 (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acids
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

20

Met Asn Gly Leu Arg His Ser Cys Asn Gln Pro Pro Gly
5 10

25

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 1930 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

	GGCACGAGCT TCGCTGTCCG CGCCCAGTGA CGCGCGTGCG GACCCGAGCC CCAATCTGCA	60
5	CCCCGCAGAC TCGCCCCCGC CCCATACCGG CGTTGCAGTC ACCGCCCGTT GCGGCCACC	120
	CCCAATGCCCGC GCGGGTCGCC CGGGCCCCGT CGCCCAATCC GCGCGGCCGGC CGCCGCCGGCC	180
10	GCTGTCTCG CTGTGGTCGC CTCTGTTGCT CTGTGTCTC GGGGTGCCTC GGGGCGGATC	240
	GGGAGCCCAC ACAGCTGTAA TCAGCCCCA GGACCCCACC CTTCTCATCG GCTCCTCCCT	300
	GCAAGCTACC TGCTCTATAAC ATGGAGACAC ACCTGGGGCC ACCGCTGAGG GGCTCTACTG	360
15	GACCCTCAAT GGTGCCGCC TGCCCTCTGA GCTGTCCCGC CTCCTTAACA CCTCCACCCCT	420
	GGCCCTGGCC CTGGCTAACCTTAATGGGTC CAGGCAGCAG TCAGGAGACA ATCTGGTGTG	480
	TCACGCCCGA GACGGCAGCA TTCTGGCTGG CTCCTGCCTC TATGTTGGCT TGCCCCCTGA	540
20	GAAGCCCTTT AACATCAGCT GCTGGTCCCG GAACATGAAG GATCTCACGT GCCGCTGGAC	600
	ACCGGGTGCA CACGGGGAGA CATTCTTACA TACCAACTAC TCCCTCAAGT ACAAGCTGAG	660
25	GTGGTACGGT CAGGATAACA CATGTGAGGA GTACCACACT GTGGGCCCTC ACTCATGCCA	720
	TATCCCCAAG GACCTGGCCC TCTTCACTCC CTATGAGATC TGGGTGGAAG CCACCAATCG	780
	CCTAGGCTCA GCAAGATCTG ATGTCCTCAC ACTGGATGTC CTGGACGTGG TGACCACGGA	840
30	CCCCCCACCC GACGTGCACG TGAGCCGCGT TGGGGCCTG GAGGACCAGC TGAGTGTGCG	900
	CTGGGTCTCA CCACCAGCTC TCAAGGATT CCTCTTCCAA GCCAAGTACC AGATCCGCTA	960
35	CCGCGTGGAG GACAGCGTGG ACTGGAAGGT GGTGGATGAC GTCAGCAACC AGACCTCCTG	1020
	CCGTCTCGCG GGCCTGAAGC CCGGCACCGT TTACTTCGTC CAAGTGCCTT GTAACCCATT	1080

	CGGGATCTAT GGGTCGAAAA AGGCAGGAAT CTGGAGCGAG TGGAGCCACC CCACCGCTGC	1140
	CTCCACCCCT CGAAGTGAGC GCCCGGGCCC GGGCGGCCGG GTGTGCGAGC CGCGGGCGG	1200
5	CGAGCCCAGC TCGGGCCCGG TGCAGCGCGA GCTCAAGCAG TTCCCTCGGCT GGCTCAAGAA	1260
	GCACGCATAC TGCTCGAACCC TTAGTTCCG CCTGTACGAC CAGTGGCGTG CTTGGATGCA	1320
	GAAGTCACAC AAGACCCGAA ACCAGGTAGG AAAGTTGGGG GAGGCTTGCG TGGGGGGTAA	1380
10	AGGAGCAGAG GAAGAGAGAG ACCCGGGTGA GCAGCCTCCA CAACACCGCA CTCTTCTTTC	1440
	CAAGCACAGG ACGAGGGGAT CCTGCCCTCG GGCAGACGGG GTGCAGCGAG AGGTAAGGGG	1500
15	GTCTGGGTGA GTGGGGCCTA CAGCAGTCTA GATGAGGCCCTTCCCTCC TTCTGGTGTG	1560
	CTCAAAGGGA TCTCTTAGTG CTCATTCAC CCACTGCAAAGAGCCCCAGG TTTTACTGCA	1620
	TCATCAAGTT GCTGAAGGGT CCAGGCTTAA TGTGGCCTCT TTTCTGCCCT CAGGTCCCTGC	1680
20	CGGCTAAACT CTAAGGATAG GCCATCCTCC TGCTGGGTCA GACCTGGAGG CTCACCTGAA	1740
	TTGGAGCCCC TCTGTACCTA TCTGGCAAC AAAGAAACCT ACCATGAGGC TGGGGCACAA	1800
25	TGAGCTCCCA CAACCACAGC TTTGGTCCAC ATGATGGTCA CACTTGGATA TACCCAGTG	1860
	TGGGTAAGGT TGGGGTATTG CAGGGCCTCC CAACAATCTC TTTAAATAAA TAAAGGAGTT	1920
	GTTCAGGTAA	1930
30		

(2) INFORMATION FOR SEQ ID NO:23:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 560 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

10	TCCAGGCAGC GGTCGGGGGA CAACCTCGTG TGCCACGCCGTGACGGCAG CATCCTGGCT	60
	GGCTCCTGCC TCTATGTTGG CCTGCCCTCA GAGAAACCCG TCAACATCAG CTGCTGGTCC	120
	AAGAACATGA AGGACTTGAC CTGCCGCTGG ACGCCAGGGG CCCACGGGGAA GACCTTCCTC	180
15	CACACCAACT ACTCCCTCAA GTACAAGCTT AGGTGGTATG GCCAGGACAA CACATGTGAG	240
	GAGTACCACCA CAGTGGGCC CCACTCCTGC CACATCCCCA AGGACCTGGC TCTCTTTACG	300
20	CCCTATGAGA TCTGGGTGGA GGCCACCAAC CGCCTGGCT CTGCCGCTC CGATGTACTC	360
	ACGCTGGATA TCCTGGATGT GGTGACCACG GACCCCCCGC CCGACGTGCA CGTGAGCCGC	420
	GTCGGGGGCC TGGAGGACCA GCTGAGCGTG CGCTGGGTGT CGCCACCCGC CCTCAAGGAT	480
25	TTCCTTTTC AAGCCAAATA CCAGATCCGC TACCGAGTGG AGGACAGTGT GGAATGGAAG	540
	GTGGTGGACG ATGTGAGCAA	560
30	(2) INFORMATION FOR SEQ ID NO:24:	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 5 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

10	ACC CTC AAC GGG CGC CGC CTG CCC CCT GAG CTC TCC CGT GTA CTC AAC	48
	Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn	
	1 5 10 15	
15	GCC TCC ACC TTG GCT CTG GCC CTG GCC AAC CTC AAT GGG TCC AGG CAG	96
	Ala Ser Thr Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln	
	20 25 30	
20	CGG TCG GGG GAC AAC CTC GTG TGC CAC GCC CGT GAC GGC AGC ATC CTG	144
	Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu	
	35 40 45	
25	GCT GGC TCC TGC CTC TAT GTT GGC CTG CCC CCA GAG AAA CCC GTC AAC	192
	Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn	
	50 55 60	
30	ATC AGC TGC TGG TCC AAG AAC ATG AAG GAC TTG ACC TGC CGC TGG ACG	240
	Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr	
	65 70 75 80	
35	CCA GGG GCC CAC GGG GAG ACC TTC CTC CAC ACC AAC TAC TCC CTC AAG	288
	Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys	
	85 90 95	
40	TAC AAG CTT AGG TGG TAT GGC CAG GAC AAC ACA TGT GAG GAG TAC CAC	336
	Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His	
	100 105 110	

	ACA GTG GGG CCC CAC TCC TGC CAC ATC CCC AAG GAC CTG GCT CTC TTT		384
	Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe		
	115	120	125
5	ACG CCC TAT GAG ATC TGG GTG GAG GCC ACC AAC CGC CTG GGC TCT GCC		432
	Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala		
	130	135	140
10	CGC TCC GAT GTA CTC ACG CTG GAT ATC CTG GAT GTG GTG ACC ACG GAC		480
	Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp		
	145	150	155
	155	160	
15	CCC CCG CCC GAC GTG CAC GTG AGC CGC GTC GGG GGC CTG GAG GAC CAG		528
	Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln		
	165	170	175
20	CTG AGC GTG CGC TGG GTG TCG CCA CCC GCC CTC AAG GAT TTC CTC TTT		576
	Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe		
	180	185	190
	190		
25	CAA GCC AAA TAC CAG ATC CGC TAC CGA GTG GAG GAC AGT GTG GAC TGG		624
	Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp		
	195	200	205
	205		
30	AAG GTG GTG GAC GAT GTG AGC AAC CAG ACC TCC TGC CGC CTG GCC GGC		672
	Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly		
	210	215	220
	220		
35	CTG AAA CCC GGC ACC GTG TAC TTC GTG CAA GTG CGC TGC AAC CCC TTT		720
	Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe		
	225	230	235
	235	240	
	240		
	GGC ATC TAT GGC TCC AAG AAA GCC GGG ATC TGG AGT GAG TGG AGC CAC		768
	Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His		
	245	250	255
	255		

	CCC ACA GCC GCC TCC ACT CCC CGC AGT GAG CGC CCG GGC CCG GGC GGC	816		
	Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly			
	260	265	270	
5	GGG GCG TGC GAA CCG CGG GGC GGA GAG CCG AGC TCG GGG CCG GTG CGG	864		
	Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg			
	275	280	285	
10	CGC GAG CTC AAG CAG TTC CTG GGC TGG CTC AAG AAG CAC GCG TAC TGC	912		
	Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys			
	290	295	300	
15	TCC AAC CTC AGC TTC CGC CTC TAC GAC CAG TGG CGA GCC TGG ATG CAG	960		
	Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln			
	305	310	315	320
20	AAG TCG CAC AAG ACC CGC AAC CAG CAC AGG ACG AGG GGA TCC TGC CCT	1008		
	Lys Ser His Lys Thr Arg Asn Gln His Arg Thr Arg Gly Ser Cys Pro			
	325	330	335	
25	CGG GCA GAC GGG GCA CGG CGA GAG GTC CTG CCA GAT AAG CTG TAGGGGCTCA	1060		
	Arg Ala Asp Gly Ala Arg Arg Glu Val Leu Pro Asp Lys Leu			
	340	345	350	
30	GGCCACCCTC CCTGCCACGT GGAGACGCAG AGGCCGAACC CAAACTGGGG CCACCTCTGT	1120		
	ACCCTCACTT CAGGGCACCT GAGCCCCTCA GCAGGGAGCTG GGGTGGCCCC TGAGCTCCAA	1180		
35	CGGCCATAAAC AGCTCTGACT CCCACGTGAG GCCACCTTTG GGTGCACCCCC AGTGGGTGTG	1240		
40	TGTGTGTGTG TGAGGGTTGG TTGAGTTGCC TAGAACCCCT GCCAGGGCTG GGGGTGAGAA	1300		
	GGGGAGTCAT TACTCCCCAT TACCTAGGGC CCCTCCAAAA GAGTCCTTTT AAATAAATGA	1360		
45	GCTATTTAGG TGCAAAAAAA AAAAAAAA A	1391		

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

5 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn
1 5 10 15

15 Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
20 25 30

Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
35 40 45

20 Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn
50 55 60

25 Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
65 70 75 80

Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
85 90 95

30 Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
100 105 110

Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
115 120 125

35 Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
130 135 140

Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp
145 150 155 160

Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln
5 165 170 175

Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe
180 185 190

10 Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp
195 200 205

Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
210 215 220

15 Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe
225 230 235 240

Gly Ile Tyr Gly Ser Lys Ala Gly Ile Trp Ser Glu Trp Ser His
20 245 250 255

Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
260 265 270

25 Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg
275 280 285

Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys
290 295 300

30 Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
305 310 315 320

Lys Ser His Lys Thr Arg Asn Gln His Arg Thr Arg Gly Ser Cys Pro
35 325 330 335

Arg Ala Asp Gly Ala Arg Arg Glu Val Leu Pro Asp Lys Leu
340 345 350

5 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCCAGGCAGC GGTGGGGGA CAAC

24

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

35 TTGCTCACAT CGTCCACCACTTTC

24

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6663 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

15	CCCAGAACTC TTGGACGCTG AGGCAGGAGG ATTCCCAAGT TTCAAGACAG TGTGTTCTA	60
	GGTAATGAGA CCCTGTCAAG AAAAGAAAAG AAATAAAGAG ACAAGAAAAT GTTTATAGGC	120
	TGTGAGACAG CTTGGTGGGT AAGGGGCACT TGCCCTCCAAT CAAGATGACC TCAGCCCCAT	180
20	CCCTAGGAAT CCATGGTAGA AGGAGAAAGC AAACTCGCAG CTGCTGACCT CCATACATGT	240
	GCTCCAATGT GCACACACAC AGGGAGACAT AATCAATTAA TAGGATGTAT TTGCTTAGAT	300
25	TTGAGTAGGC ATTTATGACT GATGTTTAA AATTTTATT TGATTTATG AAAATATACC	360
	TGTTTGTATT TGGTTGGTT TGGTTTGAGT TTTGTTTATT TGAGACAGGG CTTCTCTGTG	420
	TAGTCCTGGC TGTCCCTGGA ACTCACTCTG TAGACCAGGC TGGCCTTGAA CTCAGAAATC	480
30	CGCCTGCTTG TGCTTCCCAA GTGCTTAGAT TAAAGGTGTG CACTGCCATT CAGCAAAATT	540
	GCATACTTTA ACCCCAGTAT TTGGGAGGCA GAGGCAGACT AATGTGTGAA TTCCAGGCTA	600
35	GCCAAGGATA CAGAGTGAGA CCCTATTCTT ACCCTCCCCC CCCAAAACCC CAAAATGTAT	660
	TTTGTGCTTG TGTATGTACA TGTGTGTTGC AGCACGTAAA TGTCAGGAA CAACTTGTAG	720

	AAGTTCTCTC CGTTCACAGT CTAAGTCCTG AATTCAAAC T AAGGTCCCTCA GGCTTAGCCA	780
	CAGTCTTCTT TATGTACTGA GCCATTTCAC TGGCCCTGGA TTGACTGATG AATTAATTTT	840
5	TGAGATAAGG TCTCTTGATG CTCTAGCTAG GCTCAAAC TA TGAACTCCC AGGTCACTTT	900
	GAGCTGCTGG TACTCTTGCT TCCACCCCCA GTGGTGGAAAT GATACTCAGG CAGCACTTCT	960
	CTGGGGAAGG GGCTGGCCTT GCCCTTGATT TTGTTGCCTC AGCTTCAATG AGTGCTTGGG	1020
10	TCTCGTTGTT TCTTTCTTT ATCTGTGAAA TGGGTGAACA CCTGTTCAAG ACTTCCTGAC	1080
	TCTTGAAACA TCCAGGCAGG GTGAGGGACT TGAAAGTGGC TCATCCCAG CCTAACAAAG	1140
15	TGTCGTCTTT GACCCCAGAC ACAGCTGTAA TCAGCCCCA GGACCCCACC CTTCTCATCG	1200
	GCTCCTCCCT GCAAGCTACC TGCTCTATAC ATGGAGACAC ACCTGGGCC ACCGCTGAGG	1260
	GGCTCTACTG GACCTTCAAT GGTCGCCGCC TGCCCTCTGA GCTGTCCCGC CTCCTTAACA	1320
20	CCTCCACCCCT GGCCCTGGCC CTGGCTAAC C TTAATGGGTC CAGGCAGCAG TCAGGAGACA	1380
	ATCTGGTGTG TCACGCCGA GACGGCAGCA TTCTGGCTGG CTCCTGCCTC TATGTTGGCT	1440
25	GTAAGTGGGG CCCCAGACAC TCAGAGATAG ATGGGGTTG GCAATGACAG ATTTAGAGCC	1500
	TGGGTCTTCT GTCCTGGGCC AGAGCCATGG GCTCTCACTT GCATGCAGGC ATGGTCATAC	1560
	CCAGCACAGG CATTGCAACT CTAGGGACAG CTGTGGCTGC ACTGTCCCT GTGTACCCCA	1620
30	CAGCTTTAGA AAAGCTGTCA TGTTTCCTT GTAGTGCCCC CTGAGAAGCC CTTAACATC	1680
	AGCTGCTGGT CCCGGAACAT GAAGGATCTC ACGTGCCGCT GGACACCGGG TGCACACGGG	1740
35	GAGACATTCT TACATACCAA CTACTCCCTC AAGTACAAGC TGAGGTTGGT ACCCAGCCAA	1800
	GCCTTGCTGT GTGACTTCTG GCAATACTTA CCTTCTCTGA TCAAATATGT TCCTGTTAT	1860

	GAACCTAAAA GGGACTCTCG CACCTCCACA GGTGGTACGG TCAGGATAAC ACATGTGAGG	1920
	AGTACCACAC TGTGGGCCCT CACTCATGCC ATATCCCCAA GGACCTGGCC CTCTTCACTC	1980
5	CCTATGAGAT CTGGGTGGAA GCCACCAATC GCCTAGGCTC AGCAAGATCT GATGTCCTCA	2040
	CACTGGATGT CCTGGACGTG GGTGAGCCCC CAGTGTCCAC CTGTGTTCTG CCCTAGACCT	2100
	TATAGGGCGC CTCCCCCCC A TCCCCCAGA C TTTTGTTT CTTCTAGAGG TCTTAGCCAC	2160
10	AGCCACGGTG GTTGCAGGAC AGTGGTTGTT CATAACTTAA TGCAAAGACT TTCCCCAAG	2220
	ACAGTCAAGA TTTTCCCCCT CCCCACCCCC AACACACACA TACACACACA CTCTGCAGAG	2280
15	AACACCTGGC CTGACCACCC TCCCTCTCTA CAGCCCAGGT GTTCAGAAGG GAGTCCTAGG	2340
	GGACTGAGAG GAGGCGCCCA GGTCTGAAGG CGCCCCAGGA AGCCGAGGCC TTGAGCTGGG	2400
	GGGGGGGGCG AGGGTTGGAG GCACGAACTG GATGATCCCT GAGCACAACT GGGCTTAATC	2460
20	TAATTAGGGT GTTCCCAGCC CAAAGCAGCC TGGGCCATT AACCCTCAA GTGCCTCACT	2520
	GAAGACTCAG GGGAGAGATC AGCTTGTACT CTCTCCATGG TCCCCCAGGA GGGTCCTGG	2580
25	GTGCCCTGG CTCATTCCA CATCCAGAGG TTTTGTGTCT TCCTGGCATC TAACCCTCAG	2640
	TTGTGCTCTG TGGCTGGCAC AGCTGCCCG TGGAGGCTCT TGGTAATGTA CAAGGCATCA	2700
	GAGGTGGACA TGGGATGGGG ATACATAGGG ATGGAGCCAA ATAGCACCTC AAGGTGGGGT	2760
30	GATATACAAT AAAGCTTGTC ACCCTGACGC TCAGAAAGCC TACTCATGAT GATCACAATT	2820
	GTTGACATCA CTCTGGACA TGTAGTGAGA CCCTAGCTCA AAACACAGAC AGTAGCTTTA	2880
35	AGAGTCAGCT TGTGACTTAA TACTGGAAC CAGGGCCTAA TAGGTGCTGG GTGATGCTCG	2940
	CCTCACTCCC TGTTAGTGA GATCTCTGCG CTAATCTCCA CCCCAGCTGG GTGGGCTGCT	3000

	CTGTCCCCTT GAGGGCAGGA ATGTGTGTCT TCCATCAGAG ATAGGACCCG TGGTAGCAGC	3060
	AACTGCTGCT GGCTGTTCT GGAATATTAA ATGACAGTAA TCTATCAGGC CTGGGTGAGT	3120
5	AGCTAACAGG GGTGGGGCG TGTTCTGGAA AACGCAGATA GGGTCATAGG AGCCACTGCA	3180
	GCCTAGATTA CACCACTGGG TGTTCTGTCA CTAGGCCATT CTCACCAAGC AGTCCTCAGA	3240
	ACTGGGAGCA CTGTTGCCAG CATTAAATGC CAGCATTAA TGCCAGCATT AGGGGAGGCA	3300
10	GAGGCAGAAG GATCTCTCTG AGTTCAAGGC CATCCTGAAT TTACATAAAG AGCTCCAGGC	3360
	CAGCCAGGGT GCGCAGTAAA ACCTTGTC TC AAAAAACAAA GCATCTTAG TGACCAGGCT	3420
15	TGCTCCACCC CCAGTGACCA CGGACCCCCC ACCCGACGTG CACGTGAGCC GCGTTGGGG	3480
	CCTGGAGGAC CAGCTGAGTG TGCGCTGGGT CTCACCACCA GCTCTCAAGG ATTTCCTCTT	3540
	CCAAGCCAAG TACCAGATCC GCTACCGCGT GGAGGACAGC GTGGACTGGA AGGTGCCCGT	3600
20	CCCGCCCCGG ACCCGCCCT GACCCCGCCC CCCGCATCTG ACTCCTCCCT CACCGTGCAG	3660
	GTGGTGGATG ACGTCAGCAA CCAGACCTCC TGCCGTCTCG CGGGCCTGAA GCCCGGCACC	3720
25	GTTTACTTCG TCCAAGTGCG TTGTAACCCA TTCGGGATCT ATGGGTCGAA AAAGGCGGGA	3780
	ATCTGGAGCG AGTGGAGCCA CCCCACCGCT GCCTCCACCC CTCGAAGTGG TGAGCACCTC	3840
	TCCAGGGCTG GCTGGCCCAT GGAATCCCCA ATCCATCCTG TTCCCTCCCC CCCACCCCTT	3900
30	TTTGAGACA GCGTCTTCAG GTAGCGCATG CTGGCCTTAA ATTCAAGTATG TAGTCAAGGA	3960
	TGACCTCGAG CTCCTGGTCT TTTGTCTCC ACTTAGAGAC AATGGCCAGT GGCCATCACC	4020
35	ACCTTTGGGA GACTAGCCAT GGAGTCTATT TAGCCTGTCA TTTGGTGACA GATGGAGTAC	4080
	AACAGTGTGA CCTCTTGAA GAGAACTGAA GACAGGCTGT TTTAAACCCC AATATCCTAG	4140

	GCTCTCTAGA GGTAACTTT ATATAAAATA GAGACTATTA CAGCCAGTTA TCACATGGTC	4200
	CCACAGAACCC TTTTGTCA CAACCTATAG ACCACAGTGC CTGTGCCTAC CACATAAGGG	4260
5	TCTCTACTGC TGGCCCACCC CTCCAACCCT TAAAAGGTAA CCTAGGCAGC CTTAATATTT	4320
	GCAATCCTCC TACCTCAGCC TCTTGAATGC TCAGAAACCA GGCATTAACC CAAGTTTCTC	4380
	TTCTCTGGGT CCCTTTCTTA AGGTGGGAGG GCCTAAAGAT GACTTCCTTT GTCTGAAGA	4440
10	CTCTCCGAGC CCATGGATCT GCACTCTCTA ATATGAAATA TATTGCATAA AATGTCTGGC	4500
	CTCAGTTTCC CCACCTGTCA GGTTTAGGCA GCACAGTCGG TCCAAGACAC TTCATTATTT	4560
15	GCAGGCAGTA TAAGAAGAAG CTCCCACCCC CCACCCGCTT CCTCCGGTCC CTAAGACAGA	4620
	ATACTTCTAC ACTGAAACTG AACTCTCGCA GACGCATATG CTCACTTTAA TGATGATGAA	4680
	ATAATGGGGA AACTGAGGCT CCGAGAGATT CCTGGAGGAA GAGGGTCAAA ACCAGCTCCA	4740
20	GGAAGCTCTC CAGCCCCAT CGGGGCCTCT CCAGGTTCTG GGCTTGGCGG GAGTGAACAC	4800
	AGCTGGGAGG GGCTGGAGCC TGGGAGCTTT GGCCCTTGCT CGTGCCCAGC ACCTGCGATT	4860
25	CTTGCACGGG AGCCAGCAGG CGGCTCGTC CGCCCGAGAG ACTGAAGAAG CCGGGGGTAG	4920
	GGTTGGAGGG AGGTAAGCAG GGGCTGTGGG GGCGAAGCT TGTGCCAGGG CCTGTCAGCG	4980
	AGTCCCCAGT TTTATTTATG GCGTGAGGCC GATGTCTTTA TCCGCTGGCC TGCTGGGGGA	5040
30	TGGCTGCAGGC TGGGGATTGG ACCCAAGGGC TGGCTTCCCA CTCAGTCCTC CAGCCCAC	5100
	CATGTCACAC CCGTGCATTC TCTGAGGCTT ATCTTGGAA CCCGCCCTTG TTCTGTGCTG	5160
35	TCTGTCTCTA TTTCTGTCA TCACCTTCCC AGAGCCTTTT TTTTATGCTT TTAATATAAC	5220
	TACGTTTAA AAATTGCTTT TGTATAATGT GTGTGCCTTC GTGAGCGTGC GTGCCACAAC	5280

	ACACACGTGA AGGTTAGAGA ACTTTGTTGA GTAGGCTCCT TCCACCATGT GGGACTAGGG	5340
	CTGGCGACAA GAGCAATTAC TGAGTCATCT CGCCAGCCCC TCACCCCTCA CTTCCCATCC	5400
5	TGTTTGGATA GTCATAGGTA ATCGAAGGTA AATCGCTGGC TTTAATTTCG TAGCTATCCT	5460
	GCCTCAGCCT ACCAAGTGCT GTGCTACCAC GTTTGTGGGA GGGGCTCTCC TCCCAGTGTC	5520
	TGGGGGTGAC ACAGTCCCAA GATCTCTGCT TTCTAGGTCT TTGTCTTAGT TTGCCCTTG	5580
10	CTTTGTCCGT GTCCCTAGAG TCTCCGGCCC CACTTATCCA TTGACTGGTC TTTCCTTAC	5640
	CGAATACTCG GTTTTACCTC CCACTGATTG GACTCCCTCC TTTGCTTGTC TCCATCGCCG	5700
15	TGGCATTGCC ATTCTCTGG GTGACTCTGG GTCCACACCT GACACCTTTC CCAACTTTCC	5760
	CCAGCCGAAG CTGGTCTGGT ATGGGAGGCC GCCGTCCCAC GCGCGCCTCC TGCTGGCCGC	5820
	GCCCCAACAC TGCCGCTCCA TTCTCTTAG AGCGCCCGGG CCCGGGCGGC GGGGTGTGCG	5880
20	AGCCCGGGGG CGGCGAGCCC AGCTCGGGCC CGGTGCGGCG CGAGCTCAAG CAGTTCCTCG	5940
	GCTGGCTCAA GAAGCACGCA TACTGCTCGA ACCTTAGTTT CCGCCTGTAC GACCAGTGGC	6000
25	GTGCTTGGAT GCAGAAGTCA CACAAGACCC GAAACCAGGT AGGAAAGTTG GGGGAGGCTT	6060
	GCGTGGGGGG TAAAGGAGCA GAGGAAGAGA GAGACCCGGG TGAGCAGCCT CCACAACACC	6120
	GCACTCTTCT TTCCAAGCAC AGGACGAGGG GATCCTGCC TCGGGCAGAC GGGGTGCGGC	6180
30	GAGAGGTAAG GGGGTCTGGG TGAGTGGGC CTACAGCAGT CTAGATGAGG CCCTTCCCC	6240
	TCCTTCGGTG TTGCTCAAAG GGATCTTTA GTGCTCATTT CACCCACTGC AAAGAGCCCC	6300
35	AGGTTTTACT GCATCATCAA GTTGCTGAAG GGTCCAGGCT TAATGTGGCC TCTTTCTGC	6360
	CCTCAGGTCC TGCCGGCTAA ACTCTAAGGA TAGGCCATCC TCCTGCTGGG TCAGACCTGG	6420

AGGCTCACCT GAATTGGAGC CCCTCTGTAC CATCTGGCA ACAAAAGAAC CTACCAGAGG 6480
CTGGGCACAA TGAGCTCCC CAACCACAGC TTTGGTCCAC ATGATGGTCA CACTTGGATA 6540
5 TACCCCAGTG TGGGTAGGGT TGGGGTATTG CAGGGCCTCC CAAGAGTCTC TTTAAATAAA 6600
TAAAGGAGTT GTTCAGGTCC CGATGCCAG TGTGTTGGG GCCTATGTGC TGGGGTGGGG 6660
GGA 6663
10

(2) INFORMATION FOR SEQ ID NO:29:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

25 Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile
1 5 10 15
His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Phe
20 25 30
30 Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser
35 40 45
Thr Leu Ala Leu Ala Leu Asn Leu Asn Gly Ser Arg Gln Gln Ser
35 50 55 60

Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly
65 70 75 80

Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser
5 85 90 95

Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly
100 105 110

10 Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys
115 120 125

Leu Arg Leu Val Arg Ser Gly * His Met * Gly Val Pro His Cys
130 135 140

15 Gly Pro Ser Leu Met Pro Tyr Pro Gln Gly Pro Gly Pro Leu His Ser
145 150 155 160

Leu * Asp Leu Gly Gly Ser His Gln Ser Pro Arg Leu Ser Lys Ile
20 165 170 175

* Cys Pro His Thr Gly Cys Pro Gly Arg
180 185

25 (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGCTGGCGCG CCTCCCCGGC GGATCGGGAG CCCAC

35

5 (2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

20 AGCTACGCGT TTAGAGTTA GCCGGCAG

28

(2) INFORMATION FOR SEQ ID NO:32:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

35

Met Val Leu Ala Ser Ser Thr Thr Ser Ile His Thr Met Leu Leu Leu

1

5

10

15

Leu Leu Met Leu Phe His Leu Gly Leu Gln Ala Ser Ile Ser
20 25 30

5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

20

Ile Lys Pro Ser Gly Arg Arg Gly Ala Ala Arg Gly Pro Ala Gly Asp Tyr Lys Asp Asp
5 10 15 20

Asp Asp Lys

25

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

5 GATCTTGC_{CCC} TCGGGCAGAC GGGGTGCGGC GAGAGGT_{CCT} GCCGGCGACT ACAAGGACGA 60
CGATGACAAG TAG

73

10 (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

25

AACGGGAGCC CGTCTGCC_{CC} ACGCCGCTCT CCAGGACGGC CGCTGATGTT CCTGCTGCTA 60
CTGTTCATCC TAG

73

30

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 118 -

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCCACGCTTC TCATCGGATT CTCCCTG

27

10

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

25

CAGTCCACAC TGTCCCTCCAC TCGGTAG

27

30

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11832 base pairs
- (B) TYPE: nucleic acid
- 35 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

	GC GGCCGCTG CAGTGATTAC TCACCGCGTG GCGCACCCCA CCCGCGGGCC GCTGAGTGG	60
5	TTTTTCCGTG GGGGGATGTG AAGAAGTTA GGGAGAACTC TTCTGCACCG ATGGGAAC	120
	GGAATGCAGG GTTCGGTCCC GTTCCCCAAA GGACACACCT CTCCCCATAA GCCCACTCAT	180
	AAGGGCTCCC TGCACGCGCT CCGGGACATC CCCATATCCA ATACCCGCAG ATATGATAGT	240
10	TGAGAAGGGA CCAGAGGCCG GAGACTCCCT CCCTGCCTTC TGGCTTTCCC CCCCCCCTGC	300
	ACGAAACGAG ACTACAGCGA TGGGAGAGGT GGCATGAAGG CTTAGGGTGG GGATCGGTAG	360
15	GACCCATGCA CCCAGAGAAA GGGACTGGTG GCAACTTCA AACTCTCTGG GGAAGGAAGA	420
	AGGGCTGAAA GAGGATGAAC GGGCTCAGGT ACTGCTCAAT GTGTGTGTGG CGGACCAAAG	480
	TGGGTATGGG GGCCCCGTAAGGGGG GAAGGTGGAT AGGAAGGATC CCGGTAGACT	540
20	GGAGGGGATC CTGGAAAAGC ACCAGGGCTG CGAGCTAGGA ACCCATTCTGG AGTTAAGGGT	600
	ACAGGATCCC AGATGAGGGG GTGGGAAGCC TGGGACGGGC GGGACCAGAG AGGGAGGTCC	660
25	CACGGGCTGG TGGGAAAGA GTGGGGGGCT TCGCGCAGGA GGATGGACG TTCAGGAGTG	720
	GTAACTGGGC GGAGGCCGGC CGGGCGGGGC GCGCGGTGCC CGCGGGCGGT GGGAAAGGCCG	780
	GTGCGGGGCC CACGATCAAC CCCCCCCCCAG GGGCCGGGCC GGGCCGGGG CGGGGCCGGG	840
30	CGGGGCGAGC GGCGCATTAG CGCCTTGTCA ATTCGGCTG CTCAGACTTG CTCCGGCCTT	900
	CGCTGTCCGC GCCCAGTGAC GCGCGTGAGG ACCCGAGCCC CAATCTGCAC CCCGCAGACT	960
35	CGCCCCCGCC CCATACCGGC GTTGCAGTCA CCGCCCGTTG CGCGCCACCC CCATGCCCGC	1020
	GGGTCGCCCG GGCCCCGTG CCAAATCCGC GCGCGGCCG CGCGGCCGC TGTCCTCGCT	1080

	GTTGTCGCCT CTGTTGCTCT GTGTCCTCGG GGTGCCTCGG GGCGGATCGG GAGCCCGTGA	1140
	GTACCGTGCG CCCTGCTCCC CACCTCCCCA GGGAAGCCGG GATCCGGCGC CCCGGGGGGT	1200
5	AGTCGCGGGG GATGGAAGAA GGGGCGCGAG CGCCACCTGG ACGTCCCGGG AACAAAGGAA	1260
	GGCGGCCCTC GGGGCGCCCT CACCTGTGGG GCTCATGGCA CCACCACCCA GCCTCCCAAG	1320
	AGTACCCCGT TATACATCAG AGGCCTTTA TCTGTATCCC CTTTGCAGG CTGTCTGGCC	1380
10	AGGCTCAGTT TGAAGGACAT CGCAGTGTCC TGGGACCCCC CTCCTTCAGG GTGCTGGAC	1440
	GCTTCGGGGC GCACGCCTGT GTCTTGATA TCAGAGCGGA AGGGAAGCCT CCCTGGCCGG	1500
15	GGGCGCACGC TTGGGTGCGT TGGGTTGGGT GCTGGCGCAA AGTGGGGTCC CCTCCCCAT	1560
	GAAGTGATGA TCCCCGGGG GAGGGTGGGG CGTTATCGTG AGCCCTCCTG TCCGCCTGGC	1620
	ATGCGGCCCG GCGTCCCTCG GGACTTGCTC CTCCGTGGGG TCGGCGCCGC CCCCTCCCCC	1680
20	CTATAGCAGA CTCCATGCTT TGGTATCCTC GAAGTCCTCT CCACTGGTGG GGTCACAAC	1740
	CGGTCTCATT CAGGCTGCGC TGGGTTGAGA GCCTCTAGCG ACTGAAATT CGGTGAGGAG	1800
25	CGAGAGCAAG CGTGTCCGGG CACCGCGAGC CCAGACTTCA TTGTCTAAGG GGCACCCAGT	1860
	GGGGGTCAAG TGCCGAGAGA ATCCCACGT CCCAGGAGGA ACTCCTGGCC TTGAGCCCC	1920
	ATCACCCAAAC GCACACATCC CCGCCAGGAT GCGGTCTCCA CATCCAGACC CTCTCTGGGA	1980
30	CACACCCAAA GACACACAAA AGAGCCCCAC TGGCTTATGT CCCGTCACCC TGCCCTCCGA	2040
	CGCGCGCTGC AGCCCAGATG CGTATTGCA CACCATGCG GCGCTCGCAT TCCATCCTCT	2100
35	ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACAGAC ACGCACACAC	2160
	ACACGCACGC ACACACACGC ACGCCCGCAC TCGTGGTCCC ACATTATTT CACAGGGAG	2220

	GCAACACCGG GGTACGCATA TGGTTGAGTG CACTGGAGAT CTTTCCCCAC CACTCTCAGG	2280
	ACCCCATCCG GAGACACAGG CCACACCGCA GGGGCACCAC GCTGCGCTGC TGCTCTGGC	2340
5	TAGTAGTCTT GTGCAGTTG TCCGCGGTGT CTGTGGACGC CCTCCCGCTC TTGTCAGGGG	2400
	ACAGGAACCT ACACTCCTGC TTGCCCAAGG CGGCTGGCA GGTGATGTGG TGACACCCGG	2460
	GACCTTCCG GGGAGTTGGT GTTGCTGCCA AGCCTGGTA GTTTTGAAT GCCACCAATA	2520
10	GCGCTAACGCT TTGTTCCGG GCGGGCTGCA GAGAACAGG CGAAGGTGGC GGAGTGGGG	2580
	TGGCGCGTGT GTTTTTCTT TTAAGGGGA GAGAAATTAA ATAAGAGGTT CTCACACCTC	2640
15	TGCAATCTGT TTGTACTTAC CGTGTGTCTT AACACCTGAC CAGCCAGCCG GTGGGTCGTA	2700
	AAAGTGTATG CAGGTACCAAG CGGGACAGGA GATGGGGGCC CCTGGGTAT GGCTGGGATG	2760
	GAGGCCACCT TCCC GTTGGC CTTTCAGGGA ATCTCACACT TTTCCCTTT AAAACACATG	2820
20	GTGTTCTTT TAATAACGGC AGCAACTCCG CATTGGAAA GGGGAAATA AGCTTGTATA	2880
	GGCCCCGGCT TTGTGGAAAG GAGGGGAAGA GGGAAAGAAAA AAGGAGGGGT GTCTCCTCCA	2940
25	GGCTTAGGGG GCTGTCAGCT GCTGCTCTGT CTAGCTTGGC ATGTGTGTGC CCCAGTCCCC	3000
	AGTGGCTTTG GCCCATTGTT TGTGGAAGCC AAGAGGGAGA CTGGAGTCCT CTATCTCTGG	3060
	TACTCCAGAG TCAGGCTTCT CAGTCCGAGC CCAGAGAACG TCTTCCCTGT TTTATGGAGG	3120
30	GAATCAGGGGA AGGGGGTGCC AGGTGGACTA CGTTCTGCTG AGGACTGTAC CAGTCGCTCG	3180
	AAGGAGAAAG CTTGGGCTTG CCCCCCTCCC CCCTCAAGCC ACGAAGGGCA GCTGCTAGGC	3240
35	TAGTGTGGTA AAAGGGCATT ACTCCCCAGC CAGGACCCCC CAGAGAGTCC CCTTCCTGGC	3300
	CAGACAAATG CTGGGGAGGG ACAGAGGGGT GTGATCATTG CCCAGGAGTG CAGACAGTG	3360

	GGTCCC GG GT CGGGCAGTGC CTCCCACCC GCTGAGGGGG GCGCCCAGGC AGGAAGCGGT	3420
	GGGTGGGCCG GGGTAGAGAC GCTGGCACGT CCCAGTCAT GCCGAAGGAA TTCTGAATTA	3480
5	GCGGGCGGCT GGCTGCCTGG GACCTCCGGG GC GGCCCCCT GGCCCCCGCC GCTCCGTCTG	3540
	GCCTGCTCCT CCTGCTCCTT CGCACGGACG CTGAGACCTC CGCTGAGCCC TGGGACAAGC	3600
	CCCAAATGCA ACTGCGATTG CAGGCTTCGC AAGACCCGCC TCCTCCAAG GCCAAATTTG	3660
10	CCTGGGAGAA GTCATTCAGG GCCCAGACTA GAACCATGTT GGTGCCACCT CATCCATCTG	3720
	GGGCATGAAG GACCGTCCAG GGCTGCAGTT TAGCTTCTTA ATAGGAACCT GGGGGTGGGT	3780
15	GCAGCCTCTG TTCTCCGAGC CTCTTGAA ATCGGTTTG TTTTGTTT TGTTTTTCC	3840
	AATACTCTT TCCTCTCATC CCATCCC GGG ACTGTTTCC TCCCTAAGGG TTGAGAGCCC	3900
	TGCAGTCTTC CCTAACCTTT TCTTGCTTC TACCCCAGGG CCTTTGCACA TGGAGTCCC	3960
20	CCTCTCCCT TGCCCAACTG GGGCTCCAGC CTTACTGCAT TTGGCTCTTG GTAAGTGTCC	4020
	CAGGGCCTCT CTGACACACA GGGTTGTAGC CCCAGCTCCC TCTCTTCTCC TCCCCCCTT	4080
25	CTCTTTGCT TCTGAGACTT AATTTTTTC TTTTCTTT TGGCTTTTG AGACAGGGTT	4140
	TCTCTGTACA GCCCTGGCTG CCCTGGCACT CATTCTGTAG ACCAGGCTAG CCTCAAAC	4200
	ACAAACCTAC CTGCCTCTGC CTTTCCAGTG CTGGCACTAA AGATGTGGGC CACCACAAC	4260
30	AGTAGTTAAG TGTTTGCTG TGTCTTATT CCTATAGTGA CCTCAGTTCC TGGCATATTG	4320
	TAGGCGATGG ATGGATGAAT GGATGGATGG ATGGATGGAT GGATGGTTGG ATGGAGCAAG	4380
35	CTTGAATCGT CCTGAGTGAA AAAAGAGACC TCAGAGAACT GAATGGAGTT AGGTTCCCAG	4440
	GGCAGCCTGG CCTGCTGGTC TCATGGGAGC TCCCTGTGAA ACTTCCCCA CACCTCCCAC	4500

	CACCCGCCA TCCTGTGTGG CTGACAAGAA AGGCCAATGG CCAGATGGGG ACACAGACTC	4560
	AGGAAGCTT GGAATATGTT CCCCTCCTCA TATCCTAGGC CTTGTTGTCC CCCTGAGGGC	4620
5	CCAGCCTATG AGTAGGGCAG CTGTGGGCTG CCCTAAGGTT GGGTAGGCAA GAAGGGGGTG	4680
	GTCCCCTCAGG GTGGGTCACA GGATTGAGGT CATTCCAAA GTGGCCATCA CAGTGGCCCT	4740
	AGGAAATGAT TGTGGAGAGT CAGAACTCCT GTTGGGAGTT GTAGAGGGCC TTGCATGTGG	4800
10	GCTTCTGTGG CTGTCCCTTC TCTTGTGGTC CTTGCACAG TCCCCTCGTG TGTGCTGGGA	4860
	TGTGAGGAGG GCACGGGGAA AATGAAGGCT CAGCCCCCTCA GCTTGCCTT CACGGTTCAC	4920
15	CCAACAGGGC TCACCTCTCC TCTGGACAGG CTCTCACTGT ATGCACAGAT TGGCCTCAC	4980
	TTTGATTCCC TTCCTTGTT CTCCTGGAT GACAAACATT TACCAGGGTA GGATTTACA	5040
	TTTTAGATAT GTCCATTCTC CAGAAACACA CTTGTGAGGT TAGGGTATCA GTGAAAGGAC	5100
20	ACCACCAGGA CAGACAAAGA ATTGGAGAGG AAGGAAATTG GTAAGCCAGG CCATGCTTGA	5160
	TGGCTTATGT GTAATCCCAG AACTCTGGAC GCTGAGGCAG GAGGATTCCA AGTTCAAGA	5220
25	CAGTGTGTTTC TAGGTAATGA GACCCTGTCA AGAAAAGAAA AGAAATAAAG AGACAAGAAA	5280
	ATGTTTATAG GCTGTGAGAC AGCTTGGTGG GTAAGGGCA CTTGCCTCCA ATCAAGATGA	5340
	CCTCAGCCCC ATCCCTAGGA ATCCATGGTA GAAGGGAGAAA GCAAACCTCA GCTGCTGACC	5400
30	TCCATACATG TGCTCCAATG TGCACACACA CAGGGAGACA TAATCAATTAA ATAGGATGTA	5460
	TTTGCTTAGA TTTGAGTAGG CATTATGAC TGATGTTTA AAATTTTAT TTGATTTAT	5520
35	GAAAATATAC CTGTTGTAT TTGGTTGGT TTGGTTGAG TTTTGTAT TTGAGACAGG	5580
	GCTTCTCTGT GTAGTCCTGG CTGTCCTTGG AACTCACTCT GTAGACCAGG CTGGCCTTGA	5640

	ACTCAGAAAT CCGCCTGCTT GTGCTTCCCA AGTGCTTAGA TTAAAGGTGT GCACTGCCAT	5700
	TCAGCAAAAT TGCATACTTT AACCCCAGTA TTTGGGAGGC AGAGGCAGAC TAATGTGTGA	5760
5	ATTCCAGGCT AGCCAAGGAT ACAGAGTGAG ACCCTATTCT TACCCTCCCC CCCCAAAACC	5820
	CCAAAATGTA TTTTGTGCTT GTGTATGTAC ATGTGTGTTG CAGCACGTAATGTCCAAGG	5880
	ACAACTTGTA GAAGTTCTCT CCGTTCACAG TCTAAGTCCT GAATTCAAAC TAAGGTCCCTC	5940
10	AGGCTTAGCC ACAGTCTTCT TTATGTACTG AGCCATTCA CTGGCCCTGG ATTGACTGAT	6000
	GAATTAATTT TTGAGATAAG GTCTCTTGTAT GCTCTAGCTA GGCTCAAACATGAACTCCC	6060
15	AAGGTCATCT TGAGCTGCTG GTACTCTTGC TTCCACCCCA AGTGGTGGAA TGATACTCAG	6120
	GCAGCACTTC TCTGGGAAAG GGGCTGGCCT TGGCCTTGAT TTTGTTGCCT CAGCTTCAT	6180
	GAGTGCTTGG GTCTCGTTGT TTCTTTCTT TATCTGTGAA ATGGGTGAAC ACCTGTTCAA	6240
20	GACTTCCTGA CTCTTGAAAC ATCCAGGCAG GGTGAGGGAC TTGAAGTGGG CTCATCCCAT	6300
	GCCTAACAAA GTGTCGTCTT TGACCCCCAGA CACAGCTGTA ATCAGCCCCAGGACCCCCAC	6360
25	CCTTCTCATC GGCTCCTCCC TGCAAGCTAC CTGCTCTATA CATGGAGACA CACCTGGGGC	6420
	CACCGCTGAG GGGCTCTACT GGACCTTCAA TGGTCGCCGC CTGCCCTCTG AGCTGTCCCG	6480
	CCTCCTTAAC ACCTCCACCC TGGCCCTGGC CCTGGCTAAC CTTAATGGGT CCAGGCAGCA	6540
30	GTCAGGAGAC AATCTGGTGT GTCACGCCCG AGACGGCAGC ATTCTGGCTG GCTCCTGCCT	6600
	CTATGTTGGC TGTAAGTGGG GCCCCAGACA CTCAGAGATA GATGGGGTT GGCAATGACA	6660
35	GATTTAGAGC CTGGGTCTTC TGTCCCTGGG CAGAGCCATG GGCTCTCACT TGCAATGCAGG	6720
	CATGGTCATA CCCAGCACAG GCATTGCAAC TCTAGGGACA GCTGTGGCTG CACTGTCCCC	6780

	TGTGTACCCC ACAGCTTAG AAAAGCTGTC ATGTTTCCT TGTAGTGCCC CCTGAGAAGC	6840
	CCTTTAACAT CAGCTGCTGG TCCCGGAACA TGAAGGATCT CACGTGCCGC TGGACACCGG	6900
5	GTGCACACGG GGAGACATTG TTACATACCA ACTACTCCCT CAAGTACAAG CTGAGGTTGG	6960
	TACCCAGCCA AGCCTTGCTG TGTGACTTCT GGCAATACTT ACCTTCTCTG ATCAAATATG	7020
	TTCCTGTTA TGAACTCAAA AGGGACTCTC GCACCTCCAC AGGTGGTACG GTCAGGATAA	7080
10	CACATGTGAG GAGTACCACA CTGTGGGCC TCACTCATGC CATATCCCCA AGGACCTGGC	7140
	CCTCTTCACT CCCTATGAGA TCTGGGTGGA AGCCACCAAT CGCCTAGGCT CAGCAAGATC	7200
15	TGATGTCCTC ACACTGGATG TCCTGGACGT GGGTGAGCCC CCAGTGTCCA CCTGTGTTCT	7260
	GCCCTAGACC TTATAGGGCG CCTCCCCCCC ATCCCCCAG ACTTTTTGGT TCTTCTAGAG	7320
	GTCTTAGCCA CAGCCACGGT GGTTGCAGGA CAGTGGTTGT TCATAACTTA ATGCAAAGAC	7380
20	TTTCCCCCAA GACAGTCAAG ATTTTCCCCT CCCCACCCCC AACACACACA TACACACACA	7440
	CTCTGCAGAG AACACCTGGC CTGACCACCC TCCCTCTCTA CAGCCCAGGT GTTCAGAAGG	7500
25	GAGTCCTAGG GGACTGAGAG GAGGCGCCCA GGTCTGAAGG CGCCCCAGGA AGCCGAGGCC	7560
	TTGAGCTGGG GGGGGGGCG AGGGTTGGAG GCACGAACTG GATGATCCCT GAGCACAAC	7620
	GGGCCTAATC TAATTAGGGT GTTCCCAGCC CAAAGCAGCC TGGGCCATTT AACCCCTCAA	7680
30	GTGCCTCACT GAAGACTCAG GGGAGAGATC AGCTTGTACT CTCTCCATGG TCCCCCAGGA	7740
	GGGTTCTGG GTGCCCTGG CTCATTCCCA CATCCAGAGG TTTTGTGTCT TCCTGGCATC	7800
35	TAACCCTCAG TTGTGCTCTG TGGCTGGCAC AGCTGCCCG TGGAGGCTCT TGGTAATGTA	7860
	CAAGGCATCA GAGGTGGACA TGGGATGGGG ATACATAGGG ATGGAGCCAA ATAGCACCTC	7920

	AAGGTGGGTT GATATACAAT AAAGCTTGTC ACCCTGACGC TCAGAAAGCC TACTCATGAT	7980
	GATCACAAATT GTTGACATCA CTCTGGGACA TGTAGTGAGA CCCTAGCTCA AAACACAGAC	8040
5	AGTAGCTTTA AGAGTCAGCT TGTGACTTAA TACTGGAAC TAGGGCCTAA TAGGTGCTGG	8100
	GTGATGCTCG CCTCACTCCC TGTTTAGTGA GATCTCTGCG CTAATCTCCA CCCCAGCTGG	8160
	GTGGGCTGCT CTGTCCCCCTT GAGGGCAGGA ATGTGTGTCT TCCATCAGAG ATAGGACCCG	8220
10	TGGTAGCAGC AACTGCTGCT GGCTGTTCT GGAATATTAA ATGACAGTAA TCTATCAGGC	8280
	CTGGGTGAGT AGCTAACAGG GGTGGGGCG TGTTCTGGAA AACGCAGATA GGGTCATAGG	8340
15	AGCCACTGCA GCCTAGATTAA CACCACTGGG TGTTCTGTCA CTAGGCCATT CTCACCAAGC	8400
	AGTCCTCAGA ACTGGGAGCA CTGTTGCCAG CATTAAATGC CAGCATTAA TGCCAGCATT	8460
	AGGGGAGGCA GAGGCAGAAG GATCTCTCTG AGTTCAAGGC CATCCTGAAT TTACATAAAG	8520
20	AGCTCCAGGC CAGCCAGGGT GCGCAGTAAA ACCTTGTCTC AAAAAACAAA GCATCTTTAG	8580
	TGACCAGGCT TGCTCCACCC CCAGTGACCA CGGACCCCCC ACCCGACGTG CACGTGAGCC	8640
25	GCGTTGGGG CCTGGAGGAC CAGCTGAGTG TGCGCTGGT CTCACCACCA GCTCTCAAGG	8700
	ATTTCCCTCTT CCAAGCCAAG TACCAAGATCC GCTACCGCGT GGAGGACAGC GTGGACTGGA	8760
	AGGTGCCCGT CCCGCCCGG ACCCGCCCT GACCCCGCCC CCCGCATCTG ACTCCTCCCT	8820
30	CACCGTGCAG GTGGTGGATG ACGTCAGCAA CCAGACCTCC TGCCGTCTCG CGGGCCTGAA	8880
	GCCCCGCACC GTTTACTTCG TCCAAGTGCG TTGTAACCCA TTCGGGATCT ATGGGTCGAA	8940
35	AAAGGCAGGA ATCTGGAGCG AGTGGAGCCA CCCCACCGCT GCCTCCACCC CTCGAAGTGG	9000
	TGAGCACCTC TCCAGGGCTG GCTGGCCCAT GGAATCCCCA ATCCATCCTG TTCCCTCCCC	9060

	CCCACCCTTT TTTTGAGACA GCGTCTTCAG CTAGCGCATG CTGGCCTTAA ATTCA GTATG	9120
	TAGTCAAGGA TGACCTCGAG CTCCTGGTCT TTTTGTCTCC ACTTAGAGAC AATGCCAGT	9180
5	GGCCATCACCC ACCTTGGGA GACTAGCCAT GGAGTCTATT TAGCCTGTCA TTTGGTGACA	9240
	GATGGAGTAC AACAGTGTGA CCTCTTGTA GAGAACTGAA GACAGGCTGT TTTTAACCC	9300
	AATATCCTAG GCTCTCTAGA GTTAACTTT ATATAAAATA GAGACTATTA CAGCCAGTTA	9360
10	TCACATGGTC CCACAGAACCC TTTTGTACCA CAACCTATAG ACCACAGTGC CTGTGCCTAC	9420
	CACATAAGGG TCTCTACTGC TGGCCCACCC CTCCAACCCCT TAAAAGGTAA CCTAGGCAGC	9480
15	CTTAATATTT GCAATCCTCC TACCTCAGCC TCTTGAATGC TCAGAAACCA GGCATTAACC	9540
	CAAGTTTCTC TTCTCTGGGT CCCTTCTTA AGGTGGGAGG GCCTAAAGAT GACTTCCTTT	9600
	GTCCTGAAGA CTCTCCGAGC CCATGGATCT GCACTCTCTA ATATGAAATA TATTGCATAA	9660
20	AATGTCTGGC CTCAGTTCC CCACCTGTCA GGTTAGGCA GCACAGTCGG TCCAAGACAC	9720
	TTCATTATTT GCAGGCAGTA TAAGAAGAAG CTCCCATCCC CCACCCGCTT CCTCCGGTCC	9780
25	CTAAGACAGA ATACTTCTAC ACTGAAACTG AACTCTCGCA GACGCATATG CTCACTTTAA	9840
	TGATGATGAA ATAATGGGAA AACTGAGGCT CCGAGAGATT CCTGGAGGAA GAGGGTCAA	9900
	ACCAGCTCCA GGAAGCTCTC CAGCCCCAT CGGGCCTCT CCAGGTTCTG GGCTTGGCGG	9960
30	GAGTGAACAC AGCTGGGAGG GGCTGGAGCC TGGGAGCTTT GGCCCTTGCT CGTGCCAGC	10020
	ACCTGCGATT CTTGCACGGG AGCCAGCAGG CGGCTGCGTC CGCCCGAGAG ACTGAAGAAG	10080
35	CCGGGGGTAG GGTTGGAGGG AGGTAAGCAG GGGCTGTGGG GGCGAAGCT TGTGCCAGGG	10140
	CCTGTCAGCG AGTCCCCAGT TTTATTTATG GCGTGAGGCC GATGTCCTTA TCCGCTGGCC	10200

	TGCTGGGGGA TGGCTGCAGC TGGGGATTGG ACCCAAGGGC TGGCTTCCA CTCAGTCCTC	10260
	CAGCCCACTC CATGTCACAC CCGTGCATTC TCTGAGGCTT ATCTTGGAA CCCGCCCTTG	10320
5	TTCTGTGCTG TCTGTCTCTA TTTCTGTCTA TCACCTTCCC AGAGCCTTTT TTTTATGCTT	10380
	TTAATATAAC TACGTTTAA AAATTGCTTT TGTATAATGT GTGTGCCTTC GTGAGCGTGC	10440
	G TGCCACAAAC ACACACGTGA AGGTTAGAGA ACTTTGTTGA GTAGGCTCCT TCCACCATGT	10500
10	GGGACTAGGG CTGGCGACAA GAGCAATTAC TGAGTCATCT CGCCAGCCCC TCACCCCTCA	10560
	CTTCCCATCC TGTTGGATA GTCATAGGTA ATCGAAGGTA AATCGCTGGC TTTAATTTCG	10620
15	TAGCTATCCT GCCTCAGCCT ACCAAGTGCT GTGCTACCAC GTTTGTGGGA GGGGCTCTCC	10680
	TCCCAGTGTGTC TGGGGTACA CAGTCCCAAG ATCTCTGCTT TCTAGGTCTT TGTCTTAGTT	10740
	TGCCCCTTGC TTTGTCCGTG TCCCTAGAGT CTCCGGCCCC ACTTAGTCTC CATTGATTTC	10800
20	CTTTCTGACC GAATACTCGG TTTTACCTCC CACTGATTTG ACTCCCTCCT TTGCTTGTCT	10860
	CCATCGCCGT GGCATTGCCA TTCCTCTGGG TGACTCTGGG TCCACACCTG ACACCTTCC	10920
25	CAACTTTCCC CAGCCGAAGC TGGTCTGGTA TGGGAGGCCG CCGTCCCGCG CGCGCCTCCT	10980
	GCTGGCCCGCG CCCCCAACACT GCCGCTCCAT TCTCTTTAGA GCGCCCGGGC CGGGGCGGGCG	11040
	GGGTGTGCGA GCCGCGGGGC GGCGAGCCCA GCTCGGGCCC GGTGCGGCGC GAGCTCAAGC	11100
30	AGTTCCTCGG CTGGCTCAAG AAGCACGCAT ACTGCTCGAA CCTTAGTTTC CGCCTGTACG	11160
	ACCAGTGGCG TGCTTGGATG CAGAAGTCAC ACAAGACCCG AAACCAGGTA GGAAAGTTGG	11220
35	GGGAGGCTTG CGTGGGGGGT AAAGGAGCAG AGGAAGAGAG AGACCCGGGT GAGCAGCCTC	11280
	CACAAACACCG CACTCTTCTT TCCAAGCACA GGACGAGGGG ATCCTGCCCT CGGGCAGACG	11340

	GGGTGCGGCG AGAGGTAAGG GGGTCTGGGT GAGTGGGCC TACAGCAGTC TAGATGAGGC	11400
	CCTTTCCCT CCTTCGGTGT TGCTCAAAGG GATCTCTTAG TGCTCATTTC ACCCACTGCA	11460
5	AAGAGCCCCA GGTTTACTG CATCATCAAG TTGCTGAAGG GTCCAGGCTT AATGTGGCCT	11520
	CTTTCTGCC CTCAGGTCTT GCCGGCTAAA CTCTAAGGAT AGGCCATCCT CCTGCTGGGT	11580
	CAGACCTGGA GGCTCACCTG ATTGGAGCC CCTCTGTACC ATCTGGCAA CAAAGAAACC	11640
10	TACCAGAGGC TGGGCACAAT GAGCTCCCAC AACACAGCT TTGGTCCACA TGATGGTCAC	11700
	ACTTGGATAT ACCCCAGTGT GGGTAGGGTT GGGGTATTGC AGGGCCTCCC AAGAGTCTCT	11760
15	TTAAATAAAT AAAGGAGTTG TTCAGGTCCC GATGCCAGT GTGTTGGGG CCTATGTGCT	11820
	GGGGTGGGGG GA	11832

20 (2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acids
- 25 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

35 Val Ile Ser Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser

5

10

15

20

Ile His Gly Asp Thr Pro

25

- 131 -

CLAIMS:

1. A nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a novel haemopoietin receptor or derivative thereof having the motif:

Trp Ser Xaa Trp Ser [SEQ ID NO:1],

10 wherein Xaa is any amino acid.

2. A nucleic acid molecule according to claim 1 wherein Xaa is Asp or Glu.

15 3. A nucleic acid molecule according to claim 1 or 2 wherein said nucleic acid molecule is capable of hybridisation under low stringency conditions at 42°C to:

SN (A/G)CTCCA(A/G)TC(A/G)CTCCA 3N [SEQ ID NO:7]; and

20 SN (A/G)CTCCA(C/T)TC(A/G)CTCCA 3N [SEQ ID NO:8].

4. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:12 or a nucleotide sequence having at least 60% similarity 25 to the nucleotide sequence set forth in SEQ ID NO:12 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42°C.

30 5. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:14 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:14 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42°C.

35 6. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID

NO:16 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:16 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 421C.

5

7. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:18 or 24 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:18 or 24 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 421C.

10

8. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:28 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:28 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 421C.

15

9. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:38 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 421C.

20

10. A nucleic acid molecule according to claim 4 or 5 or 6 or 7 or 8 or 9 wherein said haemopoietin receptor is of murine origin.

25

11. A nucleic acid molecule according to claim 9 wherein said haemopoietin receptor is of human origin.

30

12. An expression vector comprising a nucleic acid molecule selected from the list consisting of:

- (i) a nucleotide sequence as set forth in SEQ ID NO:12;
- (ii) a nucleotide sequence as set forth in SEQ ID NO:14;

- (iii) a nucleotide sequence as set forth in SEQ ID NO:16;
- (iv) a nucleotide sequence as set forth in SEQ ID NO:18;
- (v) a nucleotide sequence as set forth in SEQ ID NO:24;
- (vi) a nucleotide sequence as set forth in SEQ ID NO:28; and
- 5 (vii) a nucleotide sequence as set forth in SEQ ID NO:38.

13. A method for cloning a nucleotide sequence encoding a haemopoietin receptor having the characteristics of NR6 or a derivative thereof, said method comprising searching a nucleotide database for a sequence which encodes an amino acid sequence as set forth in one or more of SEQ ID NO:1, SEQ ID NO:7 and/or SEQ ID NO:8, designing one or more oligonucleotide primers based on the nucleotide sequence located in said search, screening a nucleic acid library with said one or more oligonucleotides and obtaining a clone therefore which encodes NR6 or a part or derivative thereof.

14. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:13 or having at least about 50% similarity thereto.

15. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:15 or having at least about 50% similarity thereto.

30 16. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:17 or having at least about 50% similarity thereto.

35

17. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative

thereof having an amino acid sequence substantially as set forth in SEQ ID NO:19 or having at least about 50% similarity thereto.

5 18. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:25 or having at least about 50% similarity thereto.

10 19. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:29 or having at least about 50% similarity thereto.

15 20. An isolated novel haemopoietin receptor comprising the amino acid motif:

20 Trp Ser Xaa Trp Ser [SEQ ID NO:1]

wherein Xaa is any amino acid.

21. An isolated haemopoietin receptor according to claim 20
25 wherein Xaa is Asp or Glu.

22. An isolated haemopoietin receptor according to claim 21
comprising the amino acid sequence substantially as set forth
in SEQ ID NO:13.

30 23. An isolated haemopoietin receptor according to claim 21
comprising the amino acid sequence substantially as set forth
in SEQ ID NO:15.

35 24. An isolated haemopoietin receptor according to claim 21
comprising the amino acid sequence substantially as set forth
in SEQ ID NO:17.

25. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:19.

5 26. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:25.

10 27. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:29.

15 28. A method for modulating expression of NR6 in a mammal, said method comprising contacting a genetic sequence encoding said NR6 with an effective amount of a modulator of NR6 expression for a time and under conditions sufficient to up-regulate or down-regulate or otherwise modulate expression of NR6, wherein the genetic sequence encoding said NR6 is selected from the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 20 16 or 18 or 24 or 28 or 38 or is a sequence having at least about 60% similarity to at least one of SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 and is capable of hybridising thereto under low stringency conditions at 42°C.

25 29. A method of modulating activity of NR6 in a mammal, said method comprising administering to said mammal, a modulating effective amount of a molecule for a time and under conditions sufficient to increase or decrease NR6 activity wherein said NR6 comprises an amino acid sequence:

30 (i) encoded by a nucleotide sequence selected from the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 and which is capable of hybridising thereto under low stringency conditions at 42°C; and

35

(ii) substantially as set forth in SEQ ID NO:12 or 14 or 16 or 18 or 32 or 30 or a sequence having at least 50% similarity thereto.

5 30. A pharmaceutical composition comprising an NR6 receptor in soluble form and one or more pharmaceutically acceptable carriers and/or diluents wherein said NR6 comprises the amino acid sequence:

10 (i) encoded by a nucleotide sequence selected from the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 and which is capable of hybridising thereto under low stringency conditions at 42°C; and
15 (ii) substantially as set forth in SEQ ID NO:12 or 14 or 16 or 18 or 32 or 30 or a sequence having at least 50% similarity thereto.

20 31. An isolated antibody or a preparation of antibodies to an NR6 receptor, said NR6 receptor comprising the amino acid sequence:

25 (i) encoded by a nucleotide sequence selected from the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 and which is capable of hybridising thereto under low stringency conditions at 42°C; and
30 (ii) substantially as set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 or a sequence having at least 50% similarity thereto.

35 32. A transgenic animal comprising a mutation in at least one allele of the gene encoding NR6.

33. A transgenic animal according to claim 33 comprising a mutation in two alleles of the gene encoding NR6.

34. A transgenic animal according to claim 33 or 34 wherein
5 said animal is a murine animal.

1/43

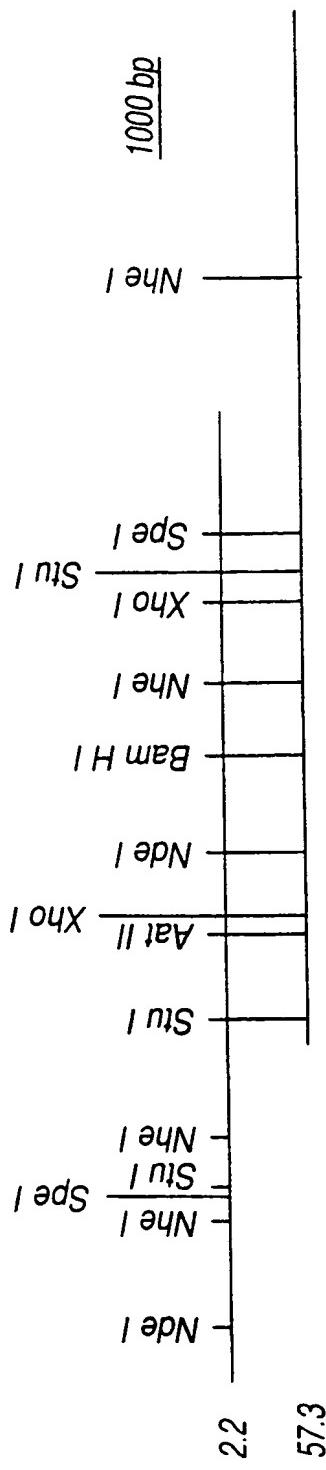
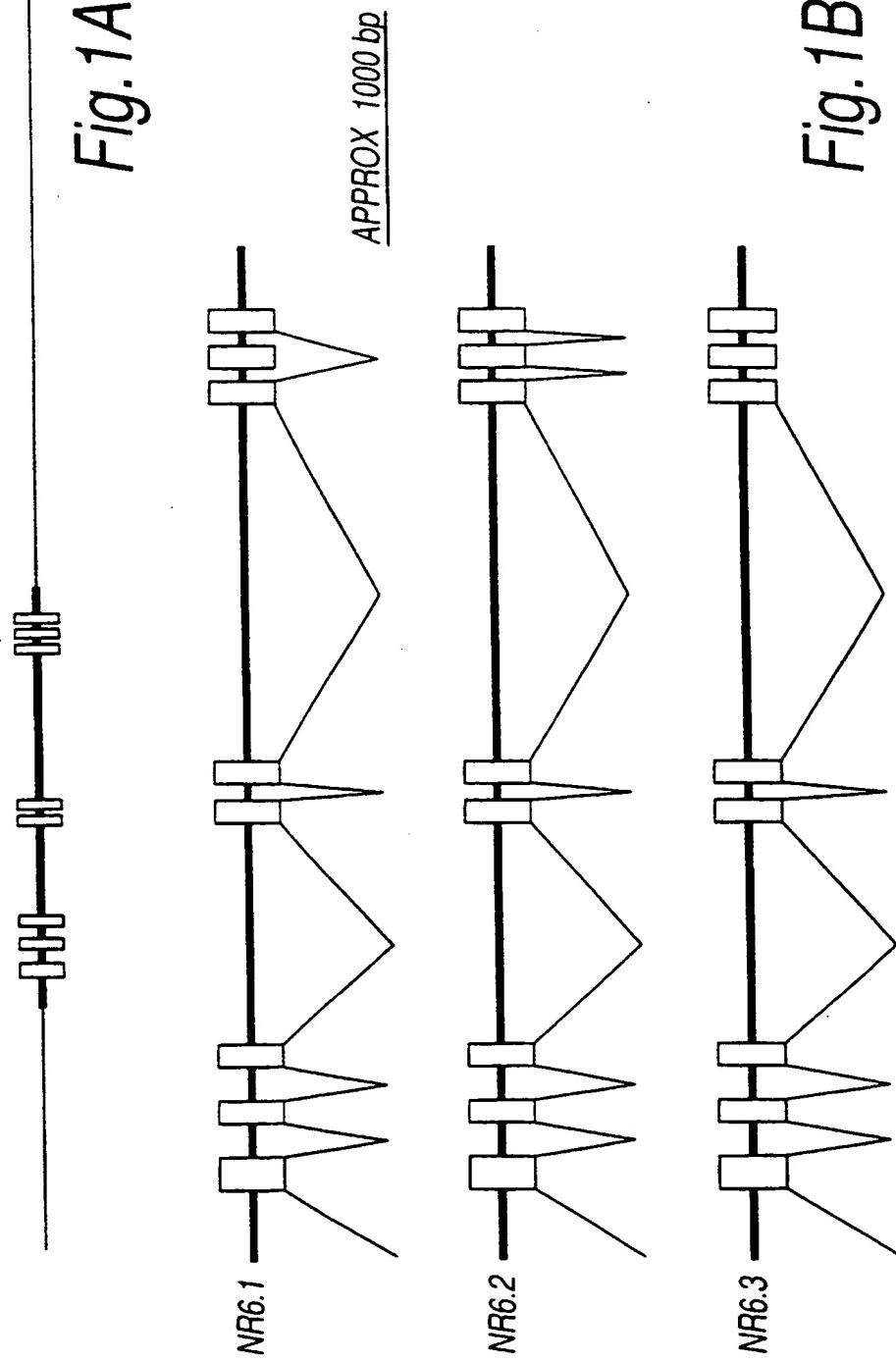


Fig. 1A



2/43

3/43	4/43
5/43	6/43
7/43	8/43
9/43	10/43
11/43	12/43
13/43	14/43
15/43	16/43
17/43	18/43

Fig.2

3/43

g1	cccaagaactct
g38	agtttcaagacagtgtgtt
g83	aagaaaagaaataaaagaga
g128	cagcttggtgggtaaggggg
g173	agccccatcccttaggaatc
g218	cagctgctgacccctccatac
g263	ggagacataatcaatttat
g308	ggcatttatgactgatgtt
g353	aatataacctgtttgtattt
g398	atttgagacaggccttc
g443	tcactctgttagaccaggct
g488	tttgtgcctcccaagtgcct
g533	gcaaaattgcataactttaa
g578	actaatgtgtgaattccag
g623	ctattcttaccctcccccc
g668	tttgttatgtacatgtgtg
g713	acttgtagaagttctctcc
g758	actaaggtcctcaggctta
g803	catttcactggccctggat
g848	aggctctttgttagctctag
g893	gtcatcttgagctgctgg
g938	aatgataactcaggcagcac
g983	ccttgattttgtgcctca
g1028	gtttctttcttatctgt
g1073	ttcctgactcttgaacat

Fig.2(i)

4/43

tggacgctgaggcaggaggattccca
tctaggtaatgagaccctgtcaagaa
caagaaaatgtttataggctgtgaga
caacttgccctccaatcaagatgacctc
catggtagaaggagaaagcaaactcg
atgtgctccaatgtgcacacacacag
aggatgtattgcttagattgagta
ttaaaaattttatggattttatgaa
ggtttggttgggttagtttttttttt
tgtgttagtcctggctgtccttggAAC
ggccttgaactcagaaatccgcctgc
agattaaagggtgtgcactgccattca
ccccagtagttgggaggcagaggcag
gctagccaaggatacagagtgagacc
ccaaaaacccaaaaatgtattttgtgc
ttgcagcacgtaaatgtccaaggaca
gttcacagtctaagtcctgaattcaa
gccacagtcttctttatgtactgagc
tgactgatgaattaattttgagata
ctaggctcaaactatgaactcccaag
actcttgcttccaccccaagtgggtgg
ttctctggggaaaggggctggccttgg
gcttcaatgagtgcttgggtctcggt
gaaatgggtgaacacacctgttcaagac
ccaggcagggtgagggacttgaagtg

Fig.2(ii)

5/43

g1118 ggctcatccatgcctaac

g1163 agctgtaatcagccccag

g1208 L Q A T C S
CCTGCAAGCTACCTGCTCT

g1253 A E G L Y W
CGCTGAGGGGCTCTACTGG

g1298 E L S R L L
TGAGCTGTCCCCGCCTCCTT

g1343 A N L N G S
GGCTAACCTTAATGGGTCC

g1388 C H A R D G
GTGTCACGCCGAGACGGC
 V G

g1433 TGTTGGCTgttaagtggggc

g1478 ttggcaatgacagat tag
 g1523 agccatgggctctcacttg
 g1568 aggcatgtcaactctagg

g1613 gtaccccacagcttttagaa

Fig.2(iii)

6/43

aaagtgtcgctttgaccccaagacac
D P T L L I G S S
GACCCCACCCCTTCATCGGCTCCTC

I H G D T P G A T
ATACATGGAGACACACCTGGGGCCAC

T F N G R R L P S
ACCTTCAATGGTGGCCGCCTGCCCTC

N T S T L A L A L
AACACCTCCACCCCTGGCCCTGGCCCT

R Q Q S G D N L V
AGGCAGCAGTCAGGAGACAATCTGGT

S I L A G S C L Y
AGCATTCTGGCTGGCTCCTGCCTCTA

cccagacactcagagatagatgggggg

agcctgggtcttctgtcctgggcag
catgcaggcatggtcataaccagcac
acagctgtggctgcactgtccccctgt

L
aagctgtcatgtttccttgttagTGC

Fig.2(iv)

7/43

	P P E K P F N
g1658	<u>CCCCTGAGAAGCCCTTAA</u>
g1703	K D L T C R W <u>AGGATCTCACGTGCCGCTG</u>
g1748	F L H T N Y S <u>TCTTACATACCAACTACTC</u>
g1793	ccagccaaggccttgctgtg
g1838	tgatcaaatatgttcctgt
g1883	W Y G cctccacacag <u>GTGGTACGGT</u>
g1928	T V G P H S <u>CACTGTGGGCCCTCACTCA</u>
g1973	F T P Y E I <u>CTTCACTCCCTATGAGATC</u>
g2018	S A R S D V <u>CTCAGCAAGATCTGATGTC</u>
g2063	tgagccccccagtgtccacc
g2108	cgcctccccccatcccccc
g2153	ttagccacagccacgggtgg
g2198	taatgcaaagactttcccc

Fig.2(v)

8/43

I S C W S R N M
CATCAGCTGCTGGTCCCGGAACATGA

T P G A H G E T
GACACCGGGTGCACACGGGGAGACAT

L K Y K L R
CCTCAAGTACAAGCTGAGgttggtac
tgacttctggcaataacttacaccttc
ttatgaactcaaaaggactctcgca

Q D N T C E E Y H
CAGGATAAACACATGTGAGGAGTACCA

C H I P K D L A L
TGCCATATCCCCAAGGACCTGGCCCT

W V E A T N R L G
TGGGTGGAAGCCACCAATCGCCTAGG

L T L D V L D V
CTCACACTGGATGTCCTGGACGTGGG

tgtgttctgccctagaccttataggg
cagacttttggttcttctagaggtc
ttgcaggacagtggttgttcataact
caagacagtcaagattttccctcc

Fig.2(vi)

9/43

g2243	ccacccccaacacacacacat
g2288	ggcctgaccaccctccctc
g2333	gtccttagggactgagagg
g2378	ggaagccgaggccttgagc
g2423	acgaactggatgatccctg
g2468	ggtgttcccagccccaaagc
g2513	gcctcactgaagactcagg
g2558	tggtcccccaggagggttc
g2603	tccagaggtttgtgtctt
g2648	ctgtggctggcacagctgc
g2693	aggcatcagaggtggacat
g2738	caaatacgacctcaaggtg
g2783	cctgacgctcagaaagcct
g2828	tcactctgggacatgttagt
g2873	tagcttaagagtcagctt
g2918	taatagggtgctgggtgatg
g2963	tctctgcgctaattctccac
g3008	cttggggcaggaatgtgt
g3053	gtagcagaactgctgctg
g3098	taatctatcaggcctgggt
g3143	gtctggaaaacgcagatag
g3188	ttacaccactgggtgttct
g3233	tcctcagaactgggagcac
g3278	taatgccagcattagggga
g3323	ttcaaggccatcctgaatt
g3368	ggtgcgcagtaaaaccttg

Fig.2(vii)

10/43

acacacacactctgcagagaacacct
tctacagcccaggtgttcagaaggga
aggcgcccaggtctgaaggcgccccca
tggggggggggggcgaggggtggaggc
agcacaactgggcctaattaaatttag
agcctggccatttaacccttcaagt
ggagagatcagctgtactctctcca
ctgggtgcccctggctcatcccaca
cctggcatctaaccctcagttgtgct
cccgtggaggctttggtaatgtaca
gggatggggatacatagggatggagc
gggtgatatacaataaaagcttgcac
actcatgatgatcacaattttgaca
gagaccctagctaaaaacacagacag
gtgacttaataactggaaactcagggcc
ctcgccctcactccctgttttagtgaga
cccagctgggtgggctgctctgtccc
gtcttccatcagagataggaccgtg
gctgtttctggaatattaaatgacag
gagtagctaacaggggtggggcggtg
ggtcataggagccactgcagcctaga
gtcactaggccattctcaccaagcag
tgttgccagcatttaatgccagcatt
ggcagaggcagaaggatctctctgag
tacataaagagctccaggccagccag
tctcaaaaaacaaagcatctttagtg

Fig.2(viii)

11/43

g3413	accaggcttgc tccacccc
g3458	V H V S R V G GTGCACGTGAGCCGCGTTG
g3503	R W V S P P CGCTGGGTCTCACCAACCAG
g3548	K Y Q I R Y <u>AAGTACCAAGATCCGCTACC</u>
g3593	gtgccccgtccccggccccggaa
g3638	ctgactcctccctcaccggt
g3683	Q T S C R L A <u>AGACCTCCTGCCGTCTCGC</u>
g3728	F V Q V R C N <u>TCGTCCAAGTGCGTTGTAA</u>
g3773	K A G I W S E AGGCGGGAAATCTGGAGCGA
g3818	T P R S <u>CCCCTCGAACGTGgtgagca</u>
g3863	aatccccaaatccatcctgt

Fig.2(ix)

SUBSTITUTE SHEET (RULE 26)

12/43

V	T	T	D	P	P	P	D
cag	TGAC	CACGGAC	CCCCC	ACCCGAC			

G	L	E	D	Q	L	S	V
GGGGC	CTGGAGG	ACCAG	CTGAGTGTg				

A	L	K	D	F	L	F	Q	A
CTCTCA	AAGG	ATT	CCT	CTT	CCA	AGCC		

R	V	E	D	S	V	D	W	K
GCGTGGAGG	ACAGCGTGG	ACTGGAA	G	cccc	ctgac	cccc	cccc	cgcat

V	V	D	D	V	S	N
gcag	<u>GTGGTGGATGACGT</u>	<u>CAGCAACC</u>				

G	L	K	P	G	T	V	Y
<u>GGGC</u>	<u>CTGAAGCCC</u>	<u>GGCACCG</u>	<u>TTACT</u>				

P	F	G	I	Y	G	S	K
<u>CCCATT</u>	<u>CGGGAT</u>	<u>CTATGGGT</u>	<u>CGAAAAA</u>				

W	S	H	P	T	A	A	S
<u>GTGGAGCC</u>	<u>ACCCCC</u>	<u>ACCG</u>	<u>GCTGC</u>	<u>CTCCA</u>			

cct	ctccagg	ggctgg	gtggccc	atgg
tcctt	cccccc	accctttt	tttgag	

Fig.2(x)

13/43

g3908	acagcgtcttcaggttagcg
g3953	gtcaaggatgacacctcgagc
g3998	gacaatggccagtgccat
g4043	agtctatttagcctgtcat
g4088	tgacctcttgcataagagaac
g4133	tatccttaggctctctagag
g4178	ttacagccagttatcacat
g4223	acctatagaccacagtgcc
g4268	tgctggcccacccctccaa
g4313	taatatttgcataatcctcct
g4358	ccaggcattaacccaagtt
g4403	gtgggagggcctaagatg
g4448	agcccatggatctgcactc
g4493	tgtctggcctcagttccc
g4538	cggtccaagacacttcatt
g4583	cccatcccccacccgcttc
g4628	tacactgaaactgaactct
g4673	atgatgaaataatggggaa
g4718	gaagaggggtcaaaaccagc
g4763	gggcctctccaggttctgg
g4808	aggggctggagcctggag
g4853	ctgcgattcttgcacggga
g4898	gagactgaagaagccgggg
g4943	gctgtggggccgaagctt
g4988	agtttatattatggcgtga
g5033	ctggggatggctgcggct

Fig.2(xi)

SUBSTITUTE SHEET (RULE 26)

14/43

catgctggccttaaattcagtagta
tcctggtctttgtctccacttaga
caccaccttggagactagccatgg
ttggtgacagatggagtacaacagtg
tgaagacaggctgttttaacccaa
gttaactttatataaaaatagagacta
ggtcccacagaacacctttgtcacaca
tgtgcctaccacataagggtctctac
cccttaaaaggtAACCTAGGCAAGCCT
acctcagccttttttttttttttttttt
tcttttttttttttttttttttttttt
acttcctttgtcctgaatgctcagaaaa
tcttttttttttttttttttttttttt
acttccctttgtcctgaagactctccg
tctaataatgaaatatattgcataaaaa
cacctgtcaggttttaggcagcacagt
atttgcaggcagtataagaagaagct
ctccggtccctaagacagaataacttc
cgcaagacgcatatgctcactttatg
actgaggctccgagagattcctggag
tccaggaagctctccagccccatcc
gcttggcgggagtgaaacacagctggg
cttggcccttgcgtcgccggcagcac
gccagcaggcggctgcgtccggccgaa
gtagggttggagggaggttaagcaggg
gtgccaggcctgtcagcgagtcggcc
ggccgatgtccttatccgctggcctg
gggattggaccgaaggctggcttc

Fig.2(xii)

SUBSTITUTE SHEET (RULE 26)

15/43

g5078	ccactcagtccctccagccc
g5123	tgaggcttatcttgggaac
g5168	ctatttctgtcattcactt
g5213	aatataactacgtttaaa
g5258	ttcgtgagcgtgcgtgcc
g5303	tttgtttagttaggctcctt
g5348	caagagcaattactgagtc
g5393	tcccatcctgtttggatag
g5438	ggcttaatttctgttagcta
g5483	gctaccacgtttgtggag
g5528	gacacagtccccaaagatctc
g5573	gccccttgctttgtccgtgt
g5618	cattgactggtcttcctt
g5663	ctgattgactccctcctt
g5708	ccattcctctgggtgactc
g5753	actttccccagccgaagct
g5798	gcgcgcgcctcctgctggc

	E	R	P	G
g5843	tcttag	<u>AGCGCCCGGGCC</u>		

	G	G	E	P	S	S
g5888	<u>GGCGGGCGAGCCCAGCTCGG</u>					
	F	L	G	W	L	K
g5933	<u>TTCCCTCGGCTGGCTCAAGA</u>					

	F	R	L	Y	D	Q
g5978	<u>TTCCGCCTGTACGACCAAGT</u>					

Fig.2(xiii)

16/43

actccatgtcacacccgtgcatttc
ccgcccttggttctgtgctgtctgtct
tcccagagccttttttatgcttt
aattgctttgtataatgtgtgtgcc
caacacacacgtgaaggtagagaac
ccaccatgtgggacttagggctggcga
atctcgccagccctcaccctcact
tcataggtaatcgaaggtaatcgct
tcctgcctcagcctaccaagtgctgt
gggcttcctccctccagtgctgtgggggt
tgctttctaggtcttgcgttttagtt
ccctagagtctccggccccacttac
taccgaataactcggttttacctccca
tgcttgcctccatcgccgtggcattg
tgggtccacacacctgacacaccttccca
ggtgtggatgggaggccgcgtccc
cgcgccccaacactgccgctccattc

P G G V C E P R
CGGGCGGCGGGGTGTGCGAGCCGCGG

G P V R R E L K Q
GCCCGGTGCGGCGCGAGCTCAAGCAG
K H A Y C S N L S
AGCACGCATACTGCTCGAACCTTAGT

W R A W M Q K S H
GGCGTGCTTGGATGCAGAAGTCACAC

Fig.2(xiv)

17/43

	K T R N Q V
g 6 0 2 3	<u>AAGACCCGAAACCAGGTAG</u>
	G K G A E E
g 6 0 6 8	<u>GGTAAAGGAGCAGAGGAAG</u>
	Q H R T L L
g 6 1 1 3	<u>CAACACCGCACTCTTCTTT</u>
	P R A D G V
g 6 1 5 8	<u>P S G R R G A</u>
g 6 2 0 3	<u>CCTCGGGCAGACGGGGTGC</u>
g 6 2 4 8	<u>GTGGGGCCTACAGCAGTCT</u>
g 6 2 9 3	<u>TGTTGCTCAAAGGGATCTC</u>
	<u>GAGCCCCAGGTTTACTGC</u>
g 6 3 3 8	CTTAATGTGGCCTCTTTTC
g 6 3 8 3	* <u>CTAAGGATAGGCCATCCTC</u>
g 6 4 2 8	CTGAATTGGAGCCCCCTCTG
g 6 4 7 3	CCAGAGGCTGGGCACAATG
g 6 5 1 8	ACATGATGGTCACACCTGG
g 6 5 6 3	GGTATTGCAGGGCCTCCCA
g 6 6 0 8	TTGTTCAGGTcccgatggc
g 6 6 5 3	ggtgtggggggaa

Fig.2(xv)

18/43

G K L G E A C V G
GAAAGTTGGGGAGGGCTTGCCTGGGG

E R D P G E Q P P
AGAGAGACCCGGGTGAGCAGCCTCCA

S K H R T R G S C
D E G I L
CCAAGCACAGGACGAGGGGATCCTGC

R R E V R G S G *
A R
GGCGAGAGGTAAGGGGTCTGGGTGA
AGATGAGGCCCTTCCCCCTCCTTCGG
TTAGTGCTCATTCACCCACTGCAAA
ATCATCAAGTTGCTGAAGGGTCCAGG

V L P A K L
G P A G *
TGCCCTCAGGTCTGCCGGCTAAACT

CTGCTGGGTCAAGACCTGGAGGCTCAC
TACCATCTGGCAACAAAGAAACCTA
AGCTCCCACAACCACAGCTTGGTCC
ATATAACCCAGTGTGGTAGGGTTGG
AGAGTCTCTTAAATAAAAGGAG
cagtgtttggggcctatgtgctgg

Fig.2(xvi)

19/43

20/43	21/43
22/43	23/43
24/43	25/43
26/43	27/43
28/43	29/43
30/43	31/43
32/43	33/43
34/43	35/43
36/43	37/43
38/43	39/43
40/43	41/43

Fig.3

SUBSTITUTE SHEET (RULE 26)

20/43

GCGGCCGCTG CAGTGATTAC TCACCGCGTG
TTTTTCCGTG GGGGGATGTG AAGAAAGTTA
GGAATGCAGG GTTCGGTCCC GTTCCCCAAA
AAGGGCTCCC TGCACGCGCT CCAGGGACATC
TGAGAAAGGGA CCAGAGGCCG GAGACTCCCT
ACGAAACGAG ACTACAGCGA TGGGAGAGGT
GACCCATGCA CCCAGAGAAA GGGACTGGTG
AGGGCTGAAA GAGGATGAAC GGGCTCAGGT
TGGGTATGGG GGCCCCGTAA GAGGGGCGGG
GGAGGGGATC CTGGAAAAGC ACCAGGGCTG
ACAGGATCCC AGATGAGGGG GTGGGAAGCC
CACGGGCTGG TGGGGAAAGA GTGGGGGGCT
GTAACTGGGC GGAGGCCGGC CGGGCGGGGC
GTGCGGGGCC CACGATCAAC CCCCCCCCCAG
CGGGGCGAGC GGCGCATTAG CGCCTTGTCA
CGCTGTCCGC GCCCAGTGAC GCGCGTGAGG
CGCCCCCGCC CCATACCGGC GTTGCAGTCA
GGGTCGCCCG GGCCCCGTG CCCAATCCGC

Fig.3(i)

SUBSTITUTE SHEET (RULE 26)

21/43

GCGCACCCCA	CCCGCGGGCC	GCTGAGTGGA	60
GGGAGAACTC	TTCTGCACCG	ATGGGAACTA	120
GGACACACCT	CTCCCCATAA	GCCCACTCAT	180
CCCATATCCA	ATACCCGCAG	ATATGATAGT	240
CCCTGCCTTC	TGGCTTCccc	CCCCCCCTGC	300
GGCATGAAGG	CTTAGGGTGG	GGATCGGTAG	360
GCAACTTCA	AACTCTCTGG	GGAAGGAAGA	420
ACTGCTCAAT	GTGTGTGTGG	CGGACCAAAG	480
GAAGGTGGAT	AGGAAGGATC	CCGGTAGACT	540
CGAGCTAGGA	ACCCATTCTGG	AGTTAAGGGT	600
TGGGACGGGC	GGGACCAGAG	AGGGAGGTCC	660
TCGCGCAGGA	GGATGGGACG	TTCAGGAGTG	720
GCGCGGTGCC	CGCGGGCGGT	GGGAAGGCCG	780
GGGCCGGGCC	GGGCCGGGGG	CGGGGCCGGG	840
ATTCGGCTG	CTCAGACTTG	CTCCGGCCTT	900
ACCCGAGCCC	CAATCTGCAC	CCCGCAGACT	960
CCGCCCGTTG	CGCGCCACCC	CCATGCCCGC	1020
CGGGCGGCCG	CCGCGGCCGC	TGTCCTCGCT	1080

Fig.3(ii)

22/43

GTGGTCGCCT CTGTTGCTCT GTGTCCTCGG
GTACCGTGCG CCCTGCTCCC CACCTCCCCA
AGTCGCGGGG GATGGAAGAA GGGGCGCGAG
GGCGGCCCTC GGGGCGCCCT CACCTGTGGG
AGTACCCCGT TATACATCAG AGGCCTCTTA
AGGCTCAGTT TGAAGGACAT CGCAGTGTCC
GCTTCGGGGC GCACGCCTGT GTCTTGGATA
GGGCGCACGC TTGGGTGCGT TGGGTTGGGT
GAAGTGATGA TCCCCGGGGG GAGGGTGGGG
ATGCGGCCCG GCGTCCCTCG GGACTTGCCT
CTATAGCAGA CTCCATGCTT TGGTATCCTC
CGGTCTCATT CAGGCTGCGC TGGGTTGAGA
CGAGAGCAAG CGTGTCCGGG CACCGCGAGC
GGGGGTCAAG TGCCGAGAGA ATCCCACTGT
ATCACCCAAC GCACACATCC CCGCCAGGAT
CACACCCAAA GACACACAAA AGAGCCCCAC
CGCGCGCTGC AGCCCAGATG CGTATTGCA
ACACACACAC ACACACACAC ACACACACAC

Fig.3(iii)

SUBSTITUTE SHEET (RULE 26)

23/43

GGTGCCTCGG	GGCGGATCGG	GAGCCCGTGA	1140
GGGAAGCCGG	GATCCGGCGC	CCCGGGGGGT	1200
CGCCACCTGG	ACGTCCCAGG	AACAAAGGAA	1260
GCTCATGGCA	CCACCAACCA	GCCTCCCAAG	1320
TCTGTATCCC	CTTGCGAGG	CTGTCTGGCC	1380
TGGGACCCCC	CTCCTTCAGG	GTGCTGGGAC	1440
TCAGAGCGGA	AGGGAAGCCT	CCCTGGCCGG	1500
GCTGGCGCAA	AGTGGGGTCC	CCTCCCCCAT	1560
CGTTATCGTG	AGCCCTCCTG	TCCGCCTGGC	1620
CTCCGTGGGG	TCGGCGCCGC	CCCCTCCCCC	1680
GAAGTCCTCT	CCACTGGTGG	GGCTCACAAAC	1740
GCCTCTAGCG	ACTGAAATT	CGGTGAGGAG	1800
CCAGACTTCA	TTGTCTAAGG	GGCACCCAGT	1860
CCCAGGAGGA	ACTCCTGGCC	TTGAGCCCCC	1920
GCGGTCTCCA	CATCCAGACC	CTCTCTGGGA	1980
TGGCTTATGT	CCCGTCACCC	TGCCCTCCGA	2040
CACCATCGCG	GCGCTCGCAT	TCCATCCTCT	2100
ACACACACAC	ACACACAGAC	ACGCACACAC	2160

Fig.3(iv)

24/43

ACACGCACGC	ACACACACGC	ACGCCCGCAC
GCAACACCCGG	GGTACGCATA	TGGTTGAGTG
ACCCCATCCG	GAGACACAGG	CCACACCGCA
TAGTAGTCTT	GTGCAGTTG	TCCGCGGTGT
ACAGGAACCT	ACACTCCTGC	TTGCCCAAGG
GACCTTCG	GGGAGTTGGT	GTTGCTGCCA
GCGCTAACGCT	TTGTTCCGG	GCAGGGCTGCA
TGGCGCGTGT	GTTTTTCTT	TTAAGGGGGA
TGCAATCTGT	TTGTACTTAC	CGTGTGTCTT
AAAGTGTATG	CAGGTACCAAG	CGGGACAGGA
GAGGCCACCT	TCCCGTTGGC	CTTCAGGGA
GTGTTCTTT	TAATAACGGC	AGCAACTCCG
GGCCCCGGCT	TTGTGGAAAG	GAGGGGAAGA
GGCTTAGGGG	GCTGTCAGCT	GCTGCTCTGT
AGTGGCTTG	GCCCATTGTT	TGTGGAAGCC
TACTCCAGAG	TCAGGCTTCT	CAGTCCGAGC
GAATCAGGGA	AGGGGGTGCC	AGGTGGACTA
AAGGAGAAAG	CTTGGGCTTG	CCCCCCTCCC

Fig.3(v)

SUBSTITUTE SHEET (RULE 26)

25/43

TCGTGGTCCC	ACATTTATTT	CACAGGGGAG	2220
CACTGGAGAT	CTTTCCCCAC	CACTCTCAGG	2280
GGGGCACCAAC	GCTGCGCTGC	TGCTCTGGGC	2340
CTGTGGACGC	CCTCCCGCTC	TTGTCAGGGG	2400
CGGCTGGGCA	GGTGATGTGG	TGACACCCGG	2460
AGCCTGGGTA	GTTTTGAAT	GCCACCAATA	2520
GAGCAACAGG	CGAAGGTGGC	GGAGTGGGGG	2580
GAGAAATTAA	ATAAGAGGTT	CTCACACCTC	2640
AACACCTGAC	CAGCCAGCCG	GTGGGTCGTA	2700
GATGGGGGCC	CCTGGGGTAT	GGCTGGGATG	2760
ATCTCACACT	TTTCCCTTTT	AAAACACATG	2820
CATTGGGAAA	GGGGGAAATA	AGCTTGTATA	2880
GGGAAGAAAA	AAGGAGGGGT	GTCTCCTCCA	2940
CTAGCTTGGC	ATGTGTGTGC	CCCAGTCCCC	3000
AAGAGGGAGA	CTGGAGTCCT	CTATCTCTGG	3060
CCAGAGAACG	TCTTCCCTGT	TTTATGGAGG	3120
CGTTCTGCTG	AGGACTGTAC	CAGTCGCTCG	3180
CCCTCAAGCC	ACGAAGGGCA	GCTGCTAGGC	3240

Fig.3(vi)

SUBSTITUTE SHEET (RULE 26)

26/43

TAGTGTGGTA AAAGGGCATT ACTCCCCAGC
CAGACAAATG CTGGGGAGGG ACAGAGGGT
GGTCCCGGGT CGGGCAGTGC CTCCCACCT
GGGTGGGCCG GGGTAGAGAC GCTGGCACGT
GCGGGCGGCT GGCTGCCTGG GACCTCCGGG
GCCTGCTCCT CCTGCTCCTT CGCACGGACG
CCCAAATGCA ACTGCGATTG CAGGCTTCGC
CCTGGGAGAA GTCATTCAGG GCCCAGACTA
GGGCATGAAG GACCGTCCAG GGCTGCAGTT
GCAGCCTCTG TTCTCCGAGC CTCTTGAA
AATACTCTT TCCTCTCATC CCATCCGGG
TGCAGTCTTC CCTAACCTTT TCTTGCTTC
CCTCTCCCCT TGCCCAACTG GGGCTCCAGC
CAGGGCCTCT CTGACACACA GGGTTGTAGC
CTCTTTGCT TCTGAGACTT AATTTTTTC
TCTCTGTACA GCCCTGGCTG CCCTGGCACT
ACAAACCTAC CTGCCTCTGC CTTCCAGTG
AGTAGTTAAG TGTTTGCTG TGTCTTATT

Fig.3(vii)

SUBSTITUTE SHEET (RULE 26)

27/43

CAGGACCCCC	CAGAGAGTCC	CCTTCCTGGC	3300
GTGATCATTG	CCCAGGAGTG	CAGACAGTGG	3360
GCTGAGGGGG	GCGCCCAGGC	AGGAAGCGGT	3420
CCCAGTTCAT	GCCGAAGGAA	TTCTGAATTA	3480
GC GGCCCCCT	GGCCCCGCC	GCTCCGTCTG	3540
CTGAGACCTC	CGCTGAGCCC	TGGGACAAGC	3600
AAGACCCGCC	TCCTCCCAAG	GCCAAATTG	3660
GAACCATGTT	GGTGCCACCT	CATCCATCTG	3720
TAGCTTCTTA	ATAGGAACCT	GGGGGTGGGT	3780
ATCGGTTTG	TTTTGTTTT	TGTTTTTTC	3840
ACTGTTTCC	TCCCTAAGGG	TTGAGAGCCC	3900
TACCCCAGGG	CCTTGACACA	TGGAGTCCA	3960
CTTACTGCAT	TTGGCTCTTG	GTAACTGTCC	4020
CCCAGCTCCC	TCTCTTCTCC	TCCCCCCCTT	4080
TTTTTCTTTT	TGGCTTTTG	AGACAGGGTT	4140
CATTCTGTAG	ACCAGGCTAG	CCTCAAAC	4200
CTGGCACTAA	AGATGTGGGC	CACCACAACT	4260
CCTATAGTGA	CCTCAGTTCC	TGGCATATTG	4320

Fig.3(viii)

SUBSTITUTE SHEET (RULE 26)

28/43

TAGGCGATGG	ATGGATGAAT	GGATGGATGG
CTTGAATCGT	CCTGAGTGAA	AAAAGAGACC
GGCAGCCTGG	CCTGCTGGTC	TCATGGGAGC
CACCCCTGCCA	TCCTGTGTGG	CTGACAAGAA
AGGGAAGCTT	GGAATATGTT	CCCCTCCTCA
CCAGCCTATG	AGTAGGGCAG	CTGTGGGCTG
GTCCCTCAGG	GTGGGTACAA	GGATTGAGGT
AGGAAATGAT	TGTGGAGAGT	CAGAACTCCT
GCTTCTGTGG	CTGTCCCTTC	TCTTGTGGTC
TGTGAGGAGG	GCACGGGGAA	AATGAAGGCT
CCAACAGGGC	TCACCTCTCC	TCTGGACAGG
TTTGATTCCC	TTCCCTTGTT	CTCCTGGGAT
TTTTAGATAT	GTCCATTCTC	CAGAACACAA
ACCACCAGGA	CAGACAAAGA	ATTGGAGAGG
TGGCTTATGT	GTAATCCCAG	AACTCTGGAC
CAGTGTGTTTC	TAGGTAATGA	GACCCTGTCA
ATGTTTATAG	GCTGTGAGAC	AGCTTGGTGG
CCTCAGCCCC	ATCCCTAGGA	ATCCATGGTA

Fig.3(ix)

SUBSTITUTE SHEET (RULE 26)

29/43

ATGGATGGAT	GGATGGTTGG	ATGGAGCAAG	4380
TCAGAGAACT	GAATGGAGTT	AGGTTCCCGAG	4440
TCCCTGTGAA	ACTTCCCCCA	CACCTCCAC	4500
AGGCCAATGG	CCAGATGGGG	ACACAGACTC	4560
TATCCTAGGC	CTTGTGTTCC	CCCTGAGGGC	4620
CCCTAACGGTT	GGGTAGGCAG	GAAGGGGGTG	4680
CATTTCCAAA	GTGGCCATCA	CAGTGGCCCT	4740
GTTGGGAGTT	GTAGAGGGCC	TTGCATGTGG	4800
CTTGCACAG	TCCCCTCGTG	TGTGCTGGGA	4860
CAGCCCCTCA	GCTTGCCCTT	CACGGTTTCAC	4920
CTCTCACTGT	ATGCACAGAT	TGGCCTCACCA	4980
GACAAACATT	TACCAGGGTA	GGATTTTACA	5040
CTTGTGAGGT	TAGGGTATCA	GTGAAAGGAC	5100
AAGGAAATTG	GTAAGCCAGG	CCATGCTTGA	5160
GCTGAGGCAG	GAGGATTCCA	AGTTTCAAGA	5220
AGAAAAGAAA	AGAAATAAAG	AGACAAGAAA	5280
GTAAGGGGCA	CTTGCCTCCA	ATCAAGATGA	5340
GAAGGAGAAA	GCAAACCTCCA	GCTGCTGACC	5400

Fig.3(x)

30/43

TCCATACATG	TGCTCCAATG	TGCACACACA
TTTGCTTAGA	TTTGAGTAGG	CATTTATGAC
GAAAATATAAC	CTGTTTGTAT	TTGGTTGGT
GCTTCTCTGT	GTAGTCCTGG	CTGTCCTTGG
ACTCAGAAAT	CCGCCTGCTT	GTGCTTCCA
TCAGCAAAAT	TGCATACTTT	AACCCCAGTA
ATTCCAGGCT	AGCCAAGGGAT	ACAGAGTGAG
CCAAAATGTA	TTTGTGCTT	GTGTATGTAC
ACAACTTGT	GAAGTTCTCT	CCGTTCACAG
AGGCTTAGCC	ACAGTCTTCT	TTATGTACTG
GAATTAATTT	TTGAGATAAG	GTCTCTTGT
AAGGTCATCT	TGAGCTGCTG	GTACTCTTGC
GCAGCACTTC	TCTGGGGAAG	GGGCTGGCCT
GAGTGCTTGG	GTCTCGTTGT	TTCTTTCTT
GACTTCCTGA	CTCTTGAAAC	ATCCAGGCAG
GCCTAACAAA	GTGTCGTCTT	TGACCCCAGA
CCTTCTCATC	GGCTCCTCCC	TGCAAGCTAC
CACCGCTGAG	GGGCTCTACT	GGACCTCAA

Fig.3(xi)

SUBSTITUTE SHEET (RULE 26)

31/43

CAGGGAGACA	TAATCAATTA	ATAGGATGTA	5460
TGATGTTTA	AAATTTTAT	TTGATTTAT	5520
TTGGTTTGAG	TTTGTTTAT	TTGAGACAGG	5580
AACTCACTCT	GTAGACCAGG	CTGGCCTTGA	5640
AGTGCTTAGA	TTAAAGGTGT	GCACTGCCAT	5700
TTTGGGAGGC	AGAGGCAGAC	TAATGTGTGA	5760
ACCCTATTCT	TACCCTCCCC	CCCCAAAACC	5820
ATGTGTGTTG	CAGCACGTAA	ATGTCCAAGG	5880
TCTAAGTCCT	GAATTCAAAC	TAAGGTCCTC	5940
AGCCATTCA	CTGGCCCTGG	ATTGACTGAT	6000
GCTCTAGCTA	GGCTCAAAC	ATGAACTCCC	6060
TTCCACCCCA	AGTGGTGGAA	TGATACTCAG	6120
TGGCCTTGAT	TTTGTTCCT	CAGCTTCAAT	6180
TATCTGTGAA	ATGGGTGAAC	ACCTGTTCAA	6240
GGTGAGGGAC	TTGAAGTGGG	CTCATCCCAT	6300
CACAGCTGTA	ATCAGCCCC	AGGACCCAC	6360
CTGCTCTATA	CATGGAGACA	CACCTGGGGC	6420
TGGTCGCCGC	CTGCCCTCTG	AGCTGTCCCG	6480

Fig.3(xii)

SUBSTITUTE SHEET (RULE 26)

32/43

CCTCCTTAAC ACCTCCACCC TGGCCCTGGC
GTCAGGAGAC AATCTGGTGT GTCACGCCCG
CTATGTTGGC TGTAAGTGGG GCCCCAGACA
GATTTAGAGC CTGGGTCTTC TGTCCCTGGGG
CATGGTCATA CCCAGCACAG GCATTGCAAC
TGTGTACCCC ACAGCTTAG AAAAGCTGTC
CCTTTAACAT CAGCTGCTGG TCCCGGAACA
GTGCACACGG GGAGACATTG TTACATACCA
TACCCAGCCA AGCCTTGCTG TGTGACTTCT
TTCCTGTTA TGAACTCAAA AGGGACTCTC
CACATGTGAG GAGTACCACA CTGTGGGCC
CCTCTTCACT CCCTATGAGA TCTGGGTGGA
TGATGTCCTC ACACTGGATG TCCTGGACGT
GCCCTAGACC TTATAGGGCG CCTCCCCCCC
GTCTTAGCCA CAGCCACGGT GGTTGCAGGA
TTTCCCCCAA GACAGTCAAG ATTTTCCCCT
CTCTGCAGAG AACACCTGGC CTGACCACCC
GAGTCCTAGG GGACTGAGAG GAGGCGCCCA

Fig.3(xiii)

33/43

CCTGGCTAAC	CTTAATGGGT	CCAGGCAGCA	6540
AGACGGCAGC	ATTCTGGCTG	GCTCCTGCCT	6600
CTCAGAGATA	GATGGGGGTT	GGCAATGACA	6660
CAGAGCCATG	GGCTCTCACT	TGCATGCAGG	6720
TCTAGGGACA	GCTGTGGCTG	CACTGTCCCC	6780
ATGTTTCCT	TGTAGTGCC	CCTGAGAAGC	6840
TGAAGGATCT	CACGTGCCGC	TGGACACCGG	6900
ACTACTCCCT	CAAGTACAAG	CTGAGGTTGG	6960
GGCAATACTT	ACCTTCTCTG	ATCAAATATG	7020
GCACCTCCAC	AGGTGGTACG	GTCAGGATAA	7080
TCACTCATGC	CATATCCCCA	AGGACCTGGC	7140
AGCCACCAAT	CGCCTAGGCT	CAGCAAGATC	7200
GGGTGAGCCC	CCAGTGTCCA	CCTGTGTTCT	7260
ATCCCCCCCAG	ACTTTTGTT	TCTTCTAGAG	7320
CAGTGGTTGT	TCATAACTTA	ATGCAAAGAC	7380
CCCCACCCCC	AACACACACA	TACACACACA	7440
TCCCTCTCTA	CAGCCCAGGT	GTTCAGAAGG	7500
GGTCTGAAGG	CGCCCCAGGA	AGCCGAGGCC	7560

Fig.3(xiv)

SUBSTITUTE SHEET (RULE 26)

34/43

TTGAGCTGGG GGGGGGGGCG AGGGTTGGAG
GGGCCTAACATC TAATTAGGGT GTTCCCAGCC
GTGCCTCACT GAAGACTCAG GGGAGAGATC
GGGTTCTGG GTGCCCTGG CTCATTCCA
TAACCCTCAG TTGTGCTCTG TGGCTGGCAC
CAAGGCATCA GAGGTGGACA TGGGATGGGG
AAGGTGGGT GATATACAAT AAAGCTTGTC
GATCACAATT GTTGACATCA CTCTGGGACA
AGTAGCTTA AGAGTCAGCT TGTGACTTAA
GTGATGCTCG CCTCACTCCC TGTTAGTGA
GTGGGCTGCT CTGTCCCCCTT GAGGGCAGGA
TGGTAGCAGC AACTGCTGCT GGCTGTTCT
CTGGGTGAGT AGCTAACAGG GGTGGGGCG
AGCCACTGCA GCCTAGATTA CACCACTGGG
AGTCCTCAGA ACTGGGAGCA CTGTTGCCAG
AGGGGAGGCA GAGGCAGAAG GATCTCTCTG
AGCTCCAGGC CAGCCAGGGT GCGCAGTAAA
TGACCAGGCT TGCTCCACCC CCAGTGACCA

Fig.3(xv)

35/43

GCACGAACTG	GATGATCCCT	GAGCACAACT	7620
CAAAGCAGCC	TGGGCCATT	AACCCTTCAA	7680
AGCTTGTACT	CTCTCCATGG	TCCCCCAGGA	7740
CATCCAGAGG	TTTTGTGTCT	TCCTGGCATC	7800
AGCTGCCCG	TGGAGGCTCT	TGGTAATGTA	7860
ATACATAGGG	ATGGAGCCAA	ATAGCACCTC	7920
ACCCTGACGC	TCAGAAAGCC	TACTCATGAT	7980
TGTAGTGAGA	CCCTAGCTCA	AAACACAGAC	8040
TACTGGAACT	CAGGGCCTAA	TAGGTGCTGG	8100
GATCTCTGCG	CTAATCTCCA	CCCCAGCTGG	8160
ATGTGTGTCT	TCCATCAGAG	ATAGGACCCG	8220
GGAATATTAA	ATGACAGTAA	TCTATCAGGC	8280
TGGTCTGGAA	AACGCAGATA	GGGTCATAGG	8340
TGTTCTGTCA	CTAGGCCATT	CTCACCAAGC	8400
CATTTAATGC	CAGCATTAA	TGCCAGCATT	8460
AGTTCAAGGC	CATCCTGAAT	TTACATAAAG	8520
ACCTTGTCTC	AAAAAAACAAA	GCATCTTAG	8580
CGGACCCCCC	ACCCGACGTG	CACGTGAGCC	8640

Fig.3(xvi)

36/43

GCGTTGGGGG CCTGGAGGAC CAGCTGAGTG
ATTCCTCTT CCAAGCCAAG TACCAGATCC
AGGTGCCCGT CCCGCCCGG ACCCGCCCT
CACCGTGCAG GTGGTGGATG ACGTCAGCAA
GCCCGGCACC GTTTACTTCG TCCAAGTGCG
AAAGGCGGGA ATCTGGAGCG AGTGGAGCCA
TGAGCACCTC TCCAGGGCTG GCTGGCCCAT
CCCACCCCTT TTTGAGACA GCGTCTTCAG
TAGTCAAGGA TGACCTCGAG CTCCTGGTCT
GGCCATCACC ACCTTTGGGA GACTAGCCAT
GATGGAGTAC AACAGTGTGA CCTCTTGTAA
AATATCCTAG GCTCTCTAGA GGTTAACCTT
TCACATGGTC CCACAGAACCC TTTTGTACCA
CACATAAGGG TCTCTACTGC TGGCCCACCC
CTTAATATTT GCAATCCTCC TACCTCAGCC
CAAGTTCTC TTCTCTGGGT CCCTTTCTTA
GTCCTGAAGA CTCTCCGAGC CCATGGATCT
AATGTCTGGC CTCAGTTCC CCACCTGTCA

Fig.3(xvii)

37/43

TGCGCTGGGT	CTCACCAACCA	GCTCTCAAGG	8700
GCTACCGCGT	GGAGGGACAGC	GTGGACTGGA	8760
GACCCCGCCC	CCCGCATCTG	ACTCCTCCCT	8820
CCAGACCTCC	TGCCGTCTCG	CGGGCCTGAA	8880
TTGTAACCCA	TTCGGGATCT	ATGGGTCGAA	8940
CCCCACCGCT	GCCTCCACCC	CTCGAAGTGG	9000
GGAATCCCCA	ATCCATCCTG	TTCCTTCCCC	9060
GTAGCGCATG	CTGGCCTTAA	ATTCAAGTATG	9120
TTTGTCCTCC	ACTTAGAGAC	AATGGCCAGT	9180
GGAGTCTATT	TAGCCTGTCA	TTTGGTGACA	9240
GAGAACTGAA	GACAGGGCTGT	TTTTAACCCC	9300
ATATAAAATA	GAGACTATTA	CAGCCAGTTA	9360
CAACCTATAG	ACCACAGTGC	CTGTGCCTAC	9420
CTCCAACCT	TAAAAGGTAA	CCTAGGCAGC	9480
TCTTGAATGC	TCAGAAACCA	GGCATTAAACC	9540
AGGTGGGAGG	GCCTAAAGAT	GACTTCCTTT	9600
GCACCTCTCA	ATATGAAATA	TATTGCATAA	9660
GGTTTAGGCA	GCACAGTCGG	TCCAAGACAC	9720

Fig.3(xviii)

38/43

TTCATTATTT GCAGGCAGTA TAAGAAGAAG
CTAAGACAGA ATACTTCTAC ACTGAAACTG
TGATGATGAA ATAATGGGGA AACTGAGGCT
ACCAGCTCCA GGAAGCTCTC CAGCCCCCAT
GAGTGAACAC AGCTGGGAGG GGCTGGAGCC
ACCTGCGATT CTTGCACGGG AGCCAGCAGG
CCGGGGGTAG GTTGGAGGG AGGTAAGCAG
CCTGTCAGCG AGTCCCCAGT TTTATTTATG
TGCTGGGGGA TGGCTGCGGC TGGGGATTGG
CAGCCCACTC CATGTACACAC CCGTGCATTC
TTCTGTGCTG TCTGTCTCTA TTTCTGTCAT
TTAATATAAC TACGTTTAA AAATTGCTTT
GTGCCACAAC ACACACGTGA AGGTTAGAGA
GGGACTAGGG CTGGCGACAA GAGCAATTAC
CTTCCCATCC TGTTTGGATA GTCATAGGTA
TAGCTATCCT GCCTCAGCCT ACCAAGTGCT
TCCCAGTGTG TGGGGGTACA CAGTCCCAAG
TGCCCCTTGC TTTGTCCGTG TCCCTAGAGT

Fig.3(xix)

SUBSTITUTE SHEET (RULE 26)

39/43

CTCCCATCCC	CCACCCGCTT	CCTCCGGTCC	9780
AACTCTCGCA	GACGCATATG	CTCACTTTAA	9840
CCGAGAGATT	CCTGGAGGAA	GAGGGTCAAA	9900
CCGGGCCTCT	CCAGGTTCTG	GGCTTGGCGG	9960
TGGGAGCTTT	GGCCCTTGCT	CGTGCCCAGC	10020
CGGCTGCGTC	CGCCCGAGAG	ACTGAAGAAG	10080
GGGCTGTGGG	GGCCGAAGCT	TGTGCCAGGG	10140
GCGTGAGGCC	GATGTCCTTA	TCCGCTGGCC	10200
ACCCAAGGGC	TGGCTTCCCA	CTCAGTCCTC	10260
TCTGAGGCTT	ATCTTGGGAA	CCCGCCCTTG	10320
TCACTTTCCC	AGAGCCTTTT	TTTTATGCTT	10380
TGTATAATGT	GTGTGCCTTC	GTGAGCGTGC	10440
ACTTTGTTGA	GTAGGCTCCT	TCCACCATGT	10500
TGAGTCATCT	CGCCAGCCCC	TCACCCCTCA	10560
ATCGAAGGTA	AATCGCTGGC	TTTAATTCG	10620
GTGCTACCAC	GTGGTGGGA	GGGGCTCTCC	10680
ATCTCTGCTT	TCTAGGTCTT	TGTCTTAGTT	10740
CTCCGGCCCC	ACTTAGTCTC	CATTGATTTTC	10800

Fig.3(xx)

SUBSTITUTE SHEET (RULE 26)

40/43

CTTTCTGACC GAATACTCGG TTTTACCTCC
CCATCGCCGT GGCATTGCCA TTCCTCTGGG
CAACTTTCCC CAGCCGAAGC TGGTCTGGTA
GCTGGCCGCG CCCCAACACT GCCGCTCCAT
GGGTGTGCGA GCCGCGGGGC GGCGAGCCA
AGTCCTCTCGG CTGGCTCAAG AAGCACGCAT
ACCAGTGGCG TGCTTGGATG CAGAAAGTCAC
GGGAGGCTTG CGTGGGGGGT AAAGGGAGCAG
CACAAACACCG CACTCTTCTT TCCAAGCACA
GGGTGCGGCG AGAGGTAAGG GGGTCTGGGT
CCTTTCCCCT CCTTCGGTGT TGCTCAAAGG
AAGAGCCCCA GGTTTTACTG CATCATCAAG
CTTTTCTGCC CTCAGGTCTT GCCGGCTAAA
CAGACCTGGA GGCTCACCTG AATTGGAGCC
TACCAGAGGC TGGGCACAAT GAGCTCCCAC
ACTTGGATAT ACCCCAGTGT GGGTAGGGTT
TTAAATAAAT AAAGGAGTTG TTCAGGTCCC
GGGGTGGGGGG GA

Fig.3(xxii)

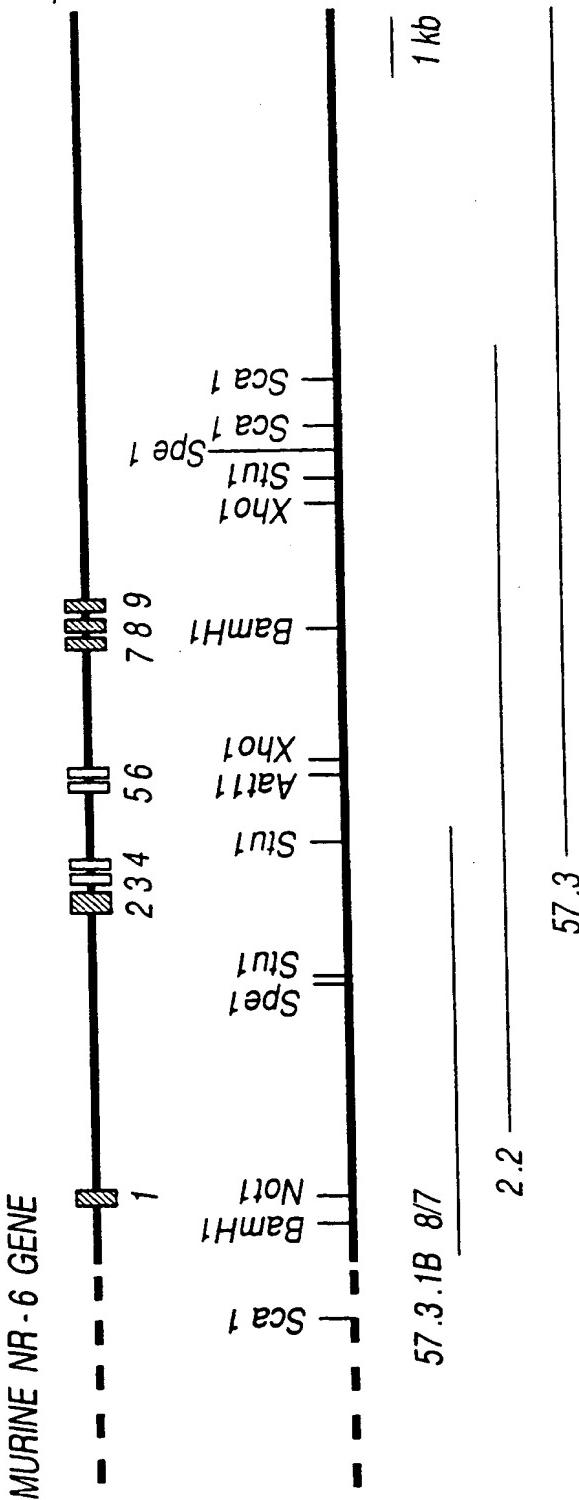
41/43

CACTGATTG	ACTCCCTCCT	TTGCTTGTCT	10860
TGACTCTGGG	TCCACACCTG	ACACCTTC	10920
TGGGAGGCCG	CCGTCCCCGCG	CGCGCCTC	10980
TCTCTTAGA	GCGCCCGGGC	CCGGGC	11040
GCTCGGGCCC	GGTGCGGC	GAGCTCAAGC	11100
ACTGCTCGAA	CCTTAGTTTC	CGCCTGTACG	11160
ACAAGACCCG	AAACCAGGTA	GGAAAGTTGG	11220
AGGAAGAGAG	AGACCCGGGT	GAGCAGC	11280
GGACGAGGGG	ATCCTGCCCT	CGGGCAGACG	11340
GAGTGGGCC	TACAGCAGTC	TAGATGAGGC	11400
GATCTCTTAG	TGCTCATTTC	ACCCACTGCA	11460
TTGCTGAAGG	GTCCAGGCTT	AATGTGGC	11520
CTCTAAGGAT	AGGCCATCCT	CCTGCTGGGT	11580
CCTCTGTACC	ATCTGGCAA	CAAAGAAACC	11640
AACCACAGCT	TTGGTCCACA	TGATGGTCAC	11700
GGGGTATTGC	AGGGCCTCCC	AAGAGTCTCT	11760
GATGGCCAGT	GTGTTGGGG	CCTATGTGCT	11820
			11832

Fig.3(xxii)

42/43

MURINE NR-6 GENOMIC STRUCTURE



LIBRARY: MOUSE 129/Sv FEMALE LIVER

MURINE NR-6 PROTEIN

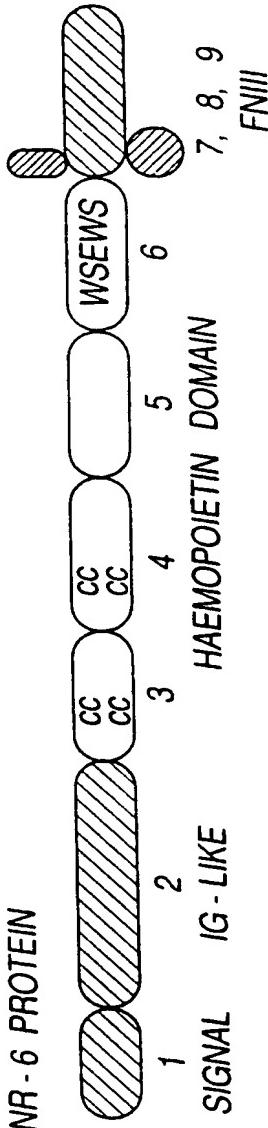


Fig. 4

43/43

TARGETING THE NR6 LOCUS BY HOMOLOGOUS RECOMBINATION

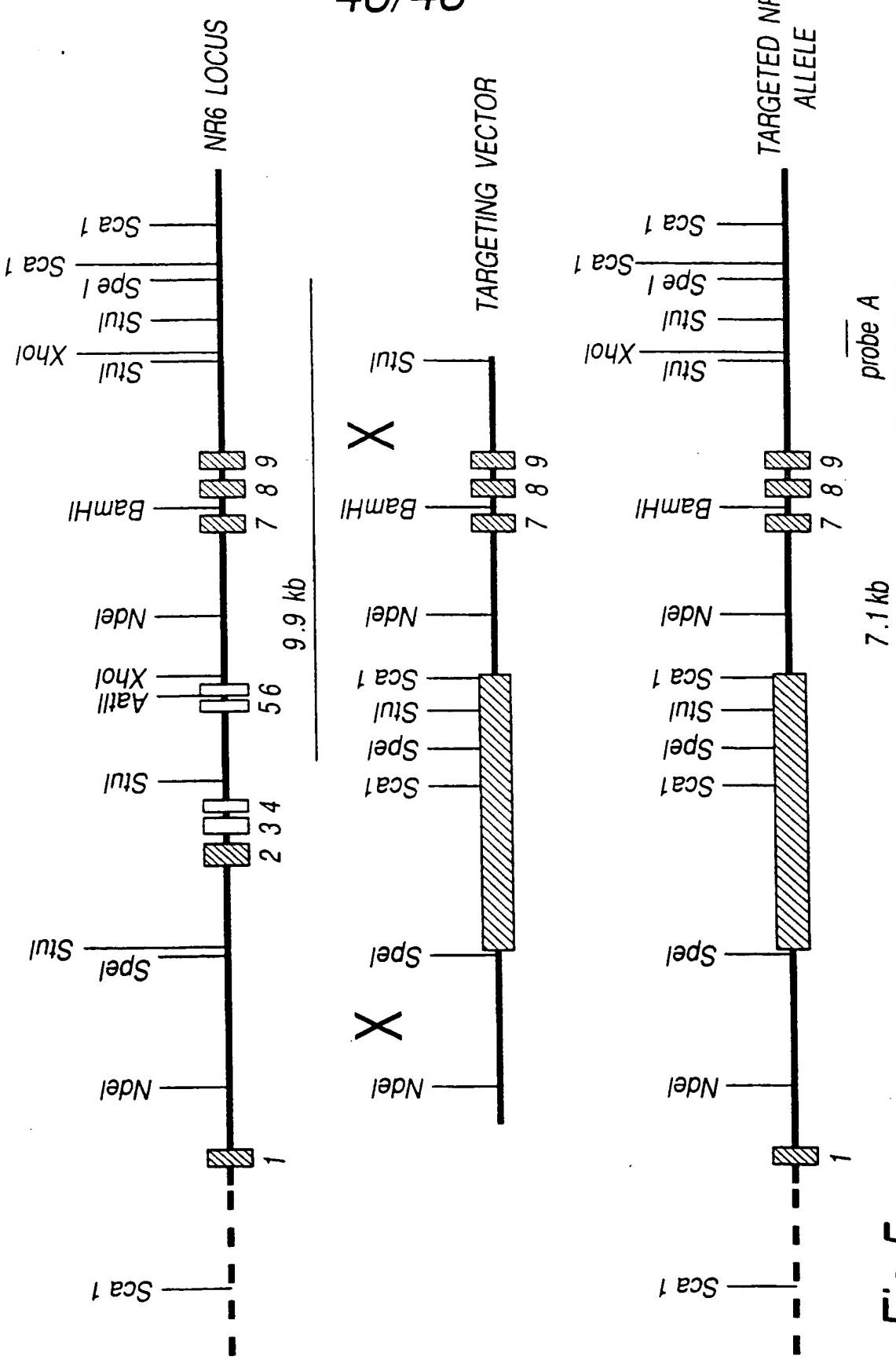


Fig. 5

INTERNATIONAL SEARCH REPORT

Internal ref.	Application No.
PCT/GB 97/02479	

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6	C12N15/19	C07K14/715	A61K38/17
C07K16/18			A01K67/027

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMEST12 emb1 SEQ ID MM77631 Acc.No:W66776, 15 June 1996 "Mus musculus cDNA mel7b11.r1 similar to PIR:B38252 granulocyte colony-stimulating factor receptor precursor" XP002055540 cited in the application & MARRA ET AL.: "The WahU-HHMI mouse EST project"</p> <p>..</p> <p>---</p> <p>-/-</p>	1-10, 14-19

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *&* document member of the same patent family

Date of the actual completion of the international search

12 February 1998

Date of mailing of the international search report

06.03.98

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Cupido, M

INTERNATIONAL SEARCH REPORT

International Application No
PCT/GB 97/02479

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ROBB ET AL.: "Structural analysis of the gene encoding the murine Interleukin-11 receptor alpha-chain and a related locus" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 271, no. 23, 7 June 1996, MD US, pages 13754-13761, XP002055539 see figure 3 ---	1-3,20, 21
X	WO 96 08510 A (PROGENITOR, INC.) 21 March 1996 see figure 2c nucleotides 1053-1068 on sheet 4/11 ---	1-3,20, 21
X	WO 96 07737 A (AMRAD OPERATIONS PTY. LTD.) 14 March 1996 see figure 8 nucleotides 1040-1055 on sheet 14/21 see claims 1,13 ---	1,3,13, 20
P,X	WO 97 15663 A (AMRAD OPERATIONS PTY. LTD.) 1 May 1997 see figure 7 (vii) on sheet 20/24 ---	1-3,20, 21
P,X	WO 97 12037 A (AMRAD OPERATIONS PTY. LTD.) 3 April 1997 see claims 1-3 ---	1-3,20, 21
P,X	WO 97 25425 A (GENENTECH, INC.) 17 July 1997 see figure 2b on sheet 12/85 -----	1-3,20, 21

INTERNATIONAL SEARCH REPORT

Inter. application No.
PCT/GB 97/02479

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
see FURTHER INFORMATION sheet PCT/ISA/210
2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
- No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/GB 97/02479

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Remark : Although claims 28 and 29 are directed to a method of treatment of the human/animal body , the search has been carried out and based on the alleged effects of the composition.

INTERNATIONAL SEARCH REPORT

Information on patent family members

Internat' l Application No

PCT/GB 97/02479

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO 9608510 A	21-03-96	US 5643748 A AU 3419495 A CA 2176463 A EP 0730606 A		01-07-97 29-03-96 21-03-96 11-09-96
WO 9607737 A	14-03-96	AU 3465295 A CA 2197873 A EP 0804576 A		27-03-96 14-03-96 05-11-97
WO 9715663 A	01-05-97	AU 7266896 A		15-05-97
WO 9712037 A	03-04-97	AU 6980596 A		17-04-97
WO 9725425 A	17-07-97	AU 1574797 A		01-08-97